



# STIC Search Report

## Biotech-Chem Library

STIC Database Tracking Number: 162513

TO: Joseph F Murphy  
Location: REM/4D78/4C70  
Art Unit: 1646  
Thursday, August 18, 2005  
  
Case Serial Number: 09/765534

From: Edward Hart  
Location: Biotech-Chem Library  
REM-1A55  
Phone: 571-272-2512  
  
edward.hart@uspto.gov

### Search Notes

Examiner Murphy,

Here are the results of the search you requested.

Please feel free to contact me if you have any questions.

Edward Hart

From: Murphy, Joseph  
Sent: Monday, August 15, 2005 11:07 AM  
To: STIC-Biotech/ChemLib  
Subject: 09765534

STIC/Biotech:

Please do an oligo search of SEQ ID NO: 2, 4.

Please include an interference search.

Please send the results on DISK.

Thanks a lot...

Joseph F. Murphy, Ph.D.  
Primary Examiner, Art Unit 1646  
joseph.murphy@uspto.gov  
Remsen 4D78  
Mailbox: 4C70  
(571) 272-0877

\*\*\*\*\*

STAFF USE ONLY

Searcher: HAA  
Searcher Phone: 2-  
Date Searcher Picked up: 8/17/05  
Date Completed: 8/17/05  
Searcher Prep/Rev. Time:         
Online Time:       

\*\*\*\*\*

Type of Search

NA#:        AA#: 2  
Interference:        SPDI:         
S/L:        Oligomer:         
Encode/Transl:         
Structure#:        Text:         
Inventor:        Litigation:       

\*\*\*\*\*

Vendors and cost where applicable

STN:         
DIALOG:         
QUESTEL/ORBIT:         
LEXIS/NEXIS:         
SEQUENCE SYSTEM: 022P  
WWW/Internet:         
Other(Specify):

# 09765534 Resultsoligo

SEQ ID NO: 2

## SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	6857	100.0	1298	2	AAR85937	Aar85937 Protein t
2	6857	100.0	1298	2	AAR90528	Aar90528 FLT4 rece
3	6857	100.0	1298	2	ADP90836	Adp90836 Human fms
4	6857	100.0	1298	3	AAY90365	Aay90365 Human Flt
5	6857	100.0	1298	3	AAY70746	Aay70746 Human tyr
6	6857	100.0	1298	5	ABG32043	Abg32043 Human Flt
7	6857	100.0	1298	6	ABU04292	Abu04292 Human exp
8	6857	100.0	1298	6	ABU04307	Abu04307 Human exp
9	6857	100.0	1298	6	ABU04296	Abu04296 Human exp
10	6857	100.0	1298	6	ABU04274	Abu04274 Human exp
11	6857	100.0	1298	6	ABU04294	Abu04294 Human exp
12	6857	100.0	1298	6	ABU04293	Abu04293 Human exp
13	6857	100.0	1298	7	ADD08956	Add08956 Human VEG
14	6857	100.0	1298	7	ADF45098	Adf45098 Human kin
15	6857	100.0	1304	6	ABU04279	Abu04279 Human exp
16	6852	99.9	1363	2	ADP90838	Adp90838 Human fms
17	6852	99.9	1363	3	AAY90366	Aay90366 Human Flt
18	6852	99.9	1363	3	AAY70747	Aay70747 Human tyr
19	6852	99.9	1363	3	AAB29047	Aab29047 Human Flt
20	6852	99.9	1363	4	AAB37604	Aab37604 Human Flt
21	6852	99.9	1363	5	ABG32044	Abg32044 Human Flt
22	6852	99.9	1363	6	ABU04297	Abu04297 Human exp
23	6852	99.9	1363	6	ABU04284	Abu04284 Human exp
24	6852	99.9	1363	6	ABU04282	Abu04282 Human exp
25	6852	99.9	1363	6	ABU04295	Abu04295 Human exp
26	6813	99.4	1298	4	AAY97785	Aay97785 Mouse Flt
27	6813	99.4	1298	4	AAY97575	Aay97575 Human Flt
28	6813	99.4	1298	6	ABU07853	Abu07853 Human vas
29	6813	99.4	1298	6	ABU04298	Abu04298 Human exp
30	6813	99.4	1298	6	ABU04304	Abu04304 Human exp
31	6813	99.4	1298	6	ABU04277	Abu04277 Human exp
32	6813	99.4	1298	7	ADN95352	Adn95352 Human BEC
33	6813	99.4	1298	8	ADQ91191	Adq91191 Human vas
34	6813	99.4	1298	8	ADR05211	Adr05211 Human fms
35	6808	99.3	1363	7	ADC64992	Adc64992 Human VEG
36	6796	99.1	1298	3	AAB30542	Aab30542 Amino aci
37	6796	99.1	1298	6	ABU04283	Abu04283 Human exp
38	6073	88.6	1363	4	AAB37607	Aab37607 Human pro
39	6073	88.6	1363	6	ABU04285	Abu04285 Human exp
40	2754.5	40.2	1356	4	AAB62475	Aab62475 Human VEG
41	2754.5	40.2	1356	4	AAY97576	Aay97576 Human Flk
42	2754.5	40.2	1356	6	ABR40196	Abr40196 Human vas
43	2754.5	40.2	1356	7	ADD08954	Add08954 Human VEG
44	2754.5	40.2	1356	7	ABM79007	Abm79007 Human VEG
45	2754.5	40.2	1356	7	ADF45097	Adf45097 Human kin

Issued Patents:

## SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	6857	100.0	1298	1	US-08-222-616-33	Sequence 33, Appl
2	6857	100.0	1298	1	US-08-340-011-2	Sequence 2, Appli
3	6857	100.0	1298	3	US-08-901-710-2	Sequence 2, Appli
4	6857	100.0	1298	3	US-08-446-648-33	Sequence 33, Appl
5	6857	100.0	1298	4	US-09-982-610-33	Sequence 33, Appl

6	6857	100.0	1298	4	US-09-169-079-2	Sequence 2, Appli
7	6857	100.0	1298	5	PCT-US95-04228-33	Sequence 33, Appl
8	6852	99.9	1363	1	US-08-340-011-4	Sequence 4, Appli
9	6852	99.9	1363	3	US-08-901-710-4	Sequence 4, Appli
10	6852	99.9	1363	4	US-09-375-248-2	Sequence 2, Appli
11	6852	99.9	1363	4	US-09-169-079-4	Sequence 4, Appli
12	6798	99.1	1363	2	US-08-874-678-32	Sequence 32, Appl
13	6798	99.1	1363	3	US-08-643-839-32	Sequence 32, Appl
14	6798	99.1	1363	3	US-09-348-886-32	Sequence 32, Appl
15	6438.5	93.9	1368	2	US-08-874-678-34	Sequence 34, Appl
16	6438.5	93.9	1368	3	US-08-643-839-34	Sequence 34, Appl
17	6438.5	93.9	1368	3	US-09-348-886-34	Sequence 34, Appl

RESULT 1

US-08-222-616-33

; Sequence 33, Application US/08222616

; Patent No. 5635177

; GENERAL INFORMATION:

; APPLICANT: Bennett, Brian D.

; APPLICANT: Goeddel, David

; APPLICANT: Lee, James M.

; APPLICANT: Matthews, William

; APPLICANT: Tsai, Siao Ping

; APPLICANT: Wood, William I.

; TITLE OF INVENTION: PROTEIN TYROSINE KINASE AGONIST

; TITLE OF INVENTION: ANTIBODIES

; NUMBER OF SEQUENCES: 42

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Genentech, Inc.

; STREET: 460 Point San Bruno Blvd

; CITY: South San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94080

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: patin (Genentech)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/222,616

; FILING DATE: 4-APR-1994

; CLASSIFICATION: 530

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/US93/00586

; FILING DATE: 22-JAN-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/826935

; FILING DATE: 22-JAN-1992

; ATTORNEY/AGENT INFORMATION:

; NAME: Lee, Wendy M.

; REGISTRATION NUMBER:

; REFERENCE/DOCKET NUMBER: 821P2

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415/225-1994

; TELEFAX: 415/952-9881

; TELEX: 910/371-7168

; INFORMATION FOR SEQ ID NO: 33:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1298 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

US-08-222-616-33

Query Match 100.0%; Score 6857; DB 1; Length 1298;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MQRGAALCLRLWLCLGLLDGLVSGYSMTPTPLNITEESHVIDTGDLSLSISCRGQHPLEWA	60
Db	1	MQRGAALCLRLWLCLGLLDGLVSGYSMTPTPLNITEESHVIDTGDLSLSISCRGQHPLEWA	60
Qy	61	WPGAQEAPATGDKDSEDGTVVRDCEGTDARPYCKVLLLHEVHANDTGSYVCYKYIKARI	120
Db	61	WPGAQEAPATGDKDSEDGTVVRDCEGTDARPYCKVLLLHEVHANDTGSYVCYKYIKARI	120
Qy	121	EGTTAASSYVFRDSEQPFINKPDTLLVNRKDMWVPLVSIPLGNVTLRSQSSVLWPDG	180
Db	121	EGTTAASSYVFRDSEQPFINKPDTLLVNRKDMWVPLVSIPLGNVTLRSQSSVLWPDG	180
Qy	181	QEVVWDDRRGMLVSTPLLDALYLQCTTWGDQDFLSNPFLVHITGNELYDIQLLPRKSL	240
Db	181	QEVVWDDRRGMLVSTPLLDALYLQCTTWGDQDFLSNPFLVHITGNELYDIQLLPRKSL	240
Qy	241	ELLVGEKLVLNCTVWAEFNSGVTFDWDYPGKQAERGKWPERRSQQTHTELSSILTIHNV	300
Db	241	ELLVGEKLVLNCTVWAEFNSGVTFDWDYPGKQAERGKWPERRSQQTHTELSSILTIHNV	300
Qy	301	SQHDLSYVCKANNGIQRFRESTEVIHNPFIISVEWLKGPILEATAGDELVKLPVKLAA	360
Db	301	SQHDLSYVCKANNGIQRFRESTEVIHNPFIISVEWLKGPILEATAGDELVKLPVKLAA	360
Qy	361	YPPPEFQWYKDGKALSGRHSPhALVLKEVTEASTGTYTALWNSAAGLRRNISLELVNV	420
Db	361	YPPPEFQWYKDGKALSGRHSPhALVLKEVTEASTGTYTALWNSAAGLRRNISLELVNV	420
Qy	421	PPQIHEKEASSPSIYSRHSRQALCTAYGVPLPLSIQWHWRPWPCKMFAQRS�RRRQOQ	480
Db	421	PPQIHEKEASSPSIYSRHSRQALCTAYGVPLPLSIQWHWRPWPCKMFAQRS�RRRQOQ	480
Qy	481	DLMQPQCRDWRAVTTQDAVNPIESLDTWTEFVEGKNKTVSKLVIQANVNSAMYKCVVSNKV	540
Db	481	DLMQPQCRDWRAVTTQDAVNPIESLDTWTEFVEGKNKTVSKLVIQANVNSAMYKCVVSNKV	540
Qy	541	GQDERLIYFYVTTIPDGFTIESKPSEELLEGGQPVLLSCQADSYKYEHLRWYRLNLSTLHD	600
Db	541	GQDERLIYFYVTTIPDGFTIESKPSEELLEGGQPVLLSCQADSYKYEHLRWYRLNLSTLHD	600
Qy	601	AHGNPLLLDCKNVHLFATPLAASLEEAPGARHATLSLSIPRVAPEHEGHYVCEVQDRRS	660
Db	601	AHGNPLLLDCKNVHLFATPLAASLEEAPGARHATLSLSIPRVAPEHEGHYVCEVQDRRS	660
Qy	661	HDKHCHKYLSVQALEAPRLTQNLTDLLVNVSDSLEMQCLVAGAHAPSIVWYKDERLLEE	720
Db	661	HDKHCHKYLSVQALEAPRLTQNLTDLLVNVSDSLEMQCLVAGAHAPSIVWYKDERLLEE	720
Qy	721	KSGVDLADSNQKLSIQRVREEDAGRYLCSVCNAKGCNVSSASVAVEGSEDKGSMEIVILV	780
Db	721	KSGVDLADSNQKLSIQRVREEDAGRYLCSVCNAKGCNVSSASVAVEGSEDKGSMEIVILV	780
Qy	781	GTGVIAVFFWVLLLLIFCNMRRPAHADIKTGYSIIMDPGEVPLEEQEYLSYDASQWEF	840
Db	781	GTGVIAVFFWVLLLLIFCNMRRPAHADIKTGYSIIMDPGEVPLEEQEYLSYDASQWEF	840
Qy	841	PRERLHLGRVLGYGAFGKVVEASAFGIHKGSSCDTVAVKMLKEGATASEHRALMSELKIL	900
Db	841	PRERLHLGRVLGYGAFGKVVEASAFGIHKGSSCDTVAVKMLKEGATASEHRALMSELKIL	900
Qy	901	IHIGNHLNVVNLGACTKPQGPLMVIIEFCKYGNLSNFLRAKRDAFSPCAEKSPEQGRF	960
Db	901	IHIGNHLNVVNLGACTKPQGPLMVIIEFCKYGNLSNFLRAKRDAFSPCAEKSPEQGRF	960
Qy	961	RAMVELARLDRRRPGSSDRVLFAFBSKTEGGARRASPDQEAEDLWLSPLTMEDLVCYSFQ	1020
Db	961	RAMVELARLDRRRPGSSDRVLFAFBSKTEGGARRASPDQEAEDLWLSPLTMEDLVCYSFQ	1020
Qy	1021	VARGMEFLASRCKIHRDLAARNILLSESDVVKICDFGLARDIYKDPDYVRKGSARLPLKW	1080
Db	1021	VARGMEFLASRCKIHRDLAARNILLSESDVVKICDFGLARDIYKDPDYVRKGSARLPLKW	1080

Qy 1081 MAPESIFDKVYTTQSDVWSFGVLLWEIFSLGASPYPGVQINEEFCQRLRDGTRMRAPELA 1140  
 |||||  
 Db 1081 MAPESIFDKVYTTQSDVWSFGVLLWEIFSLGASPYPGVQINEEFCQRLRDGTRMRAPELA 1140  
 |||||  
 Qy 1141 TPAIRIMLNCWSGDPKARPAFSELVEILGDLQGRGLQEEEEVCMAPRSSQSSEEGSFS 1200  
 |||||  
 Db 1141 TPAIRIMLNCWSGDPKARPAFSELVEILGDLQGRGLQEEEEVCMAPRSSQSSEEGSFS 1200  
 |||||  
 Qy 1201 QVSTMALHIAQADAEDSPPSLQRHSLAARYYNWVSFPGCLARGAETRGSSRMKTFEEFPM 1260  
 |||||  
 Db 1201 QVSTMALHIAQADAEDSPPSLQRHSLAARYYNWVSFPGCLARGAETRGSSRMKTFEEFPM 1260  
 |||||  
 Qy 1261 TPTTYKGSVDNQTDSGMVLASEEFEQIESRHRQESGFR 1298  
 |||||  
 Db 1261 TPTTYKGSVDNQTDSGMVLASEEFEQIESRHRQESGFR 1298  
 |||||

RESULT 4

US-08-446-648-33

; Sequence 33, Application US/08446648

; Patent No. 6331302

; GENERAL INFORMATION:

; APPLICANT: Genentech, Inc.

; APPLICANT: Bennett, Brian D.

; APPLICANT: Goeddel, David

; APPLICANT: Lee, James M.

; APPLICANT: Matthews, William

; APPLICANT: Tsai, Siao Ping

; APPLICANT: Wood, William I.

; TITLE OF INVENTION: PROTEIN TYROSINE KINASE AGONIST ANTIBODIES

; NUMBER OF SEQUENCES: 45

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Genentech, Inc.

; STREET: 460 Point San Bruno Blvd

; CITY: South San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94080

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: WinPatin (Genentech)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/446,648

; FILING DATE:

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/222616

; FILING DATE: 04-APR-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: Lee, Wendy M.

; REGISTRATION NUMBER: 40,378

; REFERENCE/DOCKET NUMBER: P0821P3PCT

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415/225-1994

; TELEFAX: 415/952-9881

; TELEX: 910/371-7168

; INFORMATION FOR SEQ ID NO: 33:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1298 amino acids

; TYPE: Amino Acid

; TOPOLOGY: Linear

US-08-446-648-33

Query Match 100.0%; Score 6857; DB 3; Length 1298;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1x 58-69, 113

7

RESULT 5

US-09-982-610-33

; Sequence 33, Application US/09982610

; Patent No. 6673343

; GENERAL INFORMATION:

; APPLICANT: Genentech, Inc.  
; Bennett, Brian D.  
; Goeddel, David  
; Lee, James M.  
; Matthews, William  
; Tsai, Siao Ping  
; Wood, William I.

; TITLE OF INVENTION: PROTEIN TYROSINE KINASE AGONIST ANTIBODIES

; NUMBER OF SEQUENCES: 45

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Genentech, Inc.  
; STREET: 460 Point San Bruno Blvd  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/982,610  
; FILING DATE: 17-Oct-2001  
; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/446,648  
; FILING DATE: 1996-MAY-23  
; APPLICATION NUMBER: 08/222616  
; FILING DATE: 04-APR-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: Lee, Wendy M.  
; REGISTRATION NUMBER: 40,378  
; REFERENCE/DOCKET NUMBER: P0821P3PCT

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415/225-1994  
; TELEFAX: 415/952-9881  
; TELEX: 910/371-7168

; INFORMATION FOR SEQ ID NO: 33:

; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1298 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear

; SEQUENCE DESCRIPTION: SEQ ID NO: 33:

US-09-982-610-33

Query Match 100.0%; Score 6857; DB 4; Length 1298;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 7

PCT-US95-04228-33

; Sequence 33, Application PC/TUS9504228

; GENERAL INFORMATION:

; APPLICANT: Genentech, Inc.  
; APPLICANT: Bennett, Brian D.  
; APPLICANT: Goeddel, David  
; APPLICANT: Lee, James M.  
; APPLICANT: Matthews, William  
; APPLICANT: Tsai, Siao Ping  
; APPLICANT: Wood, William I.

; TITLE OF INVENTION: PROTEIN TYROSINE KINASE AGONIST ANTIBODIES

; NUMBER OF SEQUENCES: 45  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Genentech, Inc.  
 ; STREET: 460 Point San Bruno Blvd  
 ; CITY: South San Francisco  
 ; STATE: California  
 ; COUNTRY: USA  
 ; ZIP: 94080  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: patin (Genentech)  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: PCT/US95/04228  
 ; FILING DATE:  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/222616  
 ; FILING DATE: 04-APR-1994  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Wendy M. Lee  
 ; REGISTRATION NUMBER: 00,000  
 ; REFERENCE/DOCKET NUMBER: 821P3PCT  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 415/225-1994  
 ; TELEFAX: 415/952-9881  
 ; TELEX: 910/371-7168  
 ; INFORMATION FOR SEQ ID NO: 33:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 1298 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 PCT-US95-04228-33

Query Match 100.0%; Score 6857; DB 5; Length 1298;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 12  
 US-08-874-678-32  
 ; Sequence 32, Application US/08874678  
 ; Patent No. 5952199  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Davis-Smyth, Terri L.  
 ; APPLICANT: Chen, Helen H.  
 ; APPLICANT: Presta, Leonard  
 ; APPLICANT: Fexrara, Napoleone  
 ; TITLE OF INVENTION: NOVEL INHIBITORS OF VASCULAR ENDOTHELIAL GROWTH FACTOR  
 ; TITLE OF INVENTION: ACTIVITY, THEIR USES AND PROCESSES FOR THEIR PRODUCTION  
 ; NUMBER OF SEQUENCES: 48  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert  
 ; STREET: Four Embarcadero Center, Suite 3400  
 ; CITY: San Francisco  
 ; STATE: California  
 ; COUNTRY: United States  
 ; ZIP: 94111-4187  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/874,678  
 ; FILING DATE: HERewith  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/643,839  
 ; FILING DATE: 07-MAY-1996

5-7-96



; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Dreger, Walter H.  
 ; REGISTRATION NUMBER: 24,190  
 ; REFERENCE/DOCKET NUMBER: A-63291-1/WH  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (415) 781-1989  
 ; TELEFAX: (415) 398-3249  
 ; TELEX: 910 277299  
 ; INFORMATION FOR SEQ ID NO: 32:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 1363 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: unknown  
 ; TOPOLOGY: unknown  
 ; MOLECULE TYPE: protein  
 US-08-874-678-32

Query Match 99.1%; Score 6798; DB 2; Length 1363;  
 Best Local Similarity 99.3%; Pred. No. 0;  
 Matches 1288; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

PGPUBS:

# SUMMARIES

Result No.	Query		DB	ID	Description
	Score	Match Length			
1	6857	100.0	1298	9	US-09-982-610-33 Sequence 33, Appl
2	6857	100.0	1298	11	US-09-765-534B-2 Sequence 2, Appli
3	6857	100.0	1298	14	US-10-262-538-32 Sequence 32, Appl
4	6857	100.0	1298	15	US-10-394-322A-67 Sequence 67, Appl
5	6857	100.0	1298	16	US-10-774-802-2 Sequence 2, Appli
6	6857	100.0	1298	16	US-10-669-176-32 Sequence 32, Appl
7	6857	100.0	1298	16	US-10-473-127-940 Sequence 940, App
8	6857	100.0	1298	16	US-10-473-127-958 Sequence 958, App
9	6857	100.0	1298	16	US-10-473-127-959 Sequence 959, App
10	6857	100.0	1298	16	US-10-473-127-960 Sequence 960, App
11	6857	100.0	1298	16	US-10-473-127-962 Sequence 962, App
12	6857	100.0	1298	16	US-10-473-127-973 Sequence 973, App
13	6857	100.0	1304	16	US-10-473-127-945 Sequence 945, App
14	6852	99.9	1363	10	US-09-375-248-2 Sequence 2, Appli
15	6852	99.9	1363	11	US-09-765-534B-4 Sequence 4, Appli
16	6852	99.9	1363	15	US-10-661-740-2 Sequence 2, Appli
17	6852	99.9	1363	16	US-10-774-802-4 Sequence 4, Appli
18	6852	99.9	1363	16	US-10-473-127-948 Sequence 948, App
19	6852	99.9	1363	16	US-10-473-127-950 Sequence 950, App
20	6852	99.9	1363	16	US-10-473-127-961 Sequence 961, App
21	6852	99.9	1363	16	US-10-473-127-963 Sequence 963, App
22	6813	99.4	1298	15	US-10-165-193A-12 Sequence 12, Appl
23	6813	99.4	1298	16	US-10-326-048-4 Sequence 4, Appli
24	6813	99.4	1298	16	US-10-473-127-943 Sequence 943, App
25	6813	99.4	1298	16	US-10-473-127-964 Sequence 964, App
26	6813	99.4	1298	16	US-10-473-127-970 Sequence 970, App
27	6813	99.4	1298	17	US-10-781-581-222 Sequence 222, App
28	6808	99.3	1363	14	US-10-081-126-2 Sequence 2, Appli
29	6798	99.1	1363	14	US-10-105-901-32 Sequence 32, Appl
30	6796	99.1	1298	16	US-10-473-127-949 Sequence 949, App
31	6438.5	93.9	1368	14	US-10-105-901-34 Sequence 34, Appl
32	6073	88.6	1363	10	US-09-375-248-19 Sequence 19, Appl
33	6073	88.6	1363	15	US-10-661-740-19 Sequence 19, Appl
34	6073	88.6	1363	16	US-10-473-127-951 Sequence 951, App
35	5646.5	82.3	1362	14	US-10-105-901-33 Sequence 33, Appl
36	4135	60.3	777	14	US-10-105-901-3 Sequence 3, Appli
37	2754.5	40.2	1356	14	US-10-090-183-2 Sequence 2, Appli
38	2754.5	40.2	1356	15	US-10-394-322A-66 Sequence 66, Appl
39	2754.5	40.2	1356	15	US-10-440-464-129 Sequence 129, App
40	2754.5	40.2	1356	16	US-10-783-528-61 Sequence 61, Appl
41	2754.5	40.2	1356	17	US-10-872-198-115 Sequence 115, App
42	2754.5	40.2	1356	17	US-10-741-600-1469 Sequence 1469, Ap

43	2754.5	40.2	1356	17	US-10-741-600-1471	Sequence 1471, Ap
44	2754.5	40.2	1356	17	US-10-926-806-10	Sequence 10, Appl
45	2754.5	40.2	1356	20	US-11-021-951-115	Sequence 115, App

RESULT 1

US-09-982-610-33

; Sequence 33, Application US/09982610

; Patent No. US20020146420A1

; GENERAL INFORMATION:

; APPLICANT: Genentech, Inc.

; Bennett, Brian D.

; Goeddel, David

; Lee, James M.

; Matthews, William

; Tsai, Siao Ping

; Wood, William I.

; TITLE OF INVENTION: PROTEIN TYROSINE KINASE AGONIST ANTIBODIES

; NUMBER OF SEQUENCES: 45

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Genentech, Inc.

; STREET: 460 Point San Bruno Blvd

; CITY: South San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94080

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: WinPatIn (Genentech)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/982,610

; FILING DATE: 17-Oct-2001

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/446,648

; FILING DATE: 1996-MAY-23

; APPLICATION NUMBER: 08/222616

; FILING DATE: 04-APR-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: Lee, Wendy M.

; REGISTRATION NUMBER: 40,378

; REFERENCE/DOCKET NUMBER: P0821P3PCT

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415/225-1994

; TELEFAX: 415/952-9881

; TELEX: 910/371-7168

; INFORMATION FOR SEQ ID NO: 33:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1298 amino acids

; TYPE: Amino Acid

; TOPOLOGY: Linear

; SEQUENCE DESCRIPTION: SEQ ID NO: 33:

US-09-982-610-33

Query Match 100.0%; Score 6857; DB 9; Length 1298;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 4

US-10-394-322A-67

; Sequence 67, Application US/10394322A

; Publication No. US20030232391A1

; GENERAL INFORMATION:

; APPLICANT: SUNESIS PHARMACEUTICALS, INC.

; APPLICANT: Prescott, John C.

; TITLE OF INVENTION: IDENTIFICATION OF KINASE INHIBITORS

; FILE REFERENCE: 39750-0006 US  
; CURRENT APPLICATION NUMBER: US/10/394,322A  
; CURRENT FILING DATE: 2003-03-20  
; PRIOR APPLICATION NUMBER: US 60/366,892  
; PRIOR FILING DATE: 2002-03-21  
; NUMBER OF SEQ ID NOS: 70  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 67  
; LENGTH: 1298  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-394-322A-67

Query Match 100.0%; Score 6857; DB 15; Length 1298;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 10  
US-10-473-127-960  
; Sequence 960, Application US/10473127  
; Publication No. US20040236091A1  
; GENERAL INFORMATION:  
; APPLICANT: Zycos Inc.  
; TITLE OF INVENTION: TRANSLATIONAL PROFILING  
; FILE REFERENCE: 08191-026W01  
; CURRENT APPLICATION NUMBER: US/10/473,127  
; CURRENT FILING DATE: 2003-09-26  
; PRIOR APPLICATION NUMBER: 60/279,495  
; PRIOR FILING DATE: 2001-03-28  
; PRIOR APPLICATION NUMBER: 60/292,544  
; PRIOR FILING DATE: 2001-05-21  
; PRIOR APPLICATION NUMBER: 60/310,801  
; PRIOR FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: 60/326,370  
; PRIOR FILING DATE: 2001-10-01  
; PRIOR APPLICATION NUMBER: 60/336,780  
; PRIOR FILING DATE: 2001-12-04  
; PRIOR APPLICATION NUMBER: 60/358,985  
; PRIOR FILING DATE: 2002-02-20  
; NUMBER OF SEQ ID NOS: 2041  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 960  
; LENGTH: 1298  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-473-127-960

3-28-01

Query Match 100.0%; Score 6857; DB 16; Length 1298;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

# SEQ ID NO: 4

## SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	7211	100.0	1363	2	ADP90838	Adp90838 Human fms
2	7211	100.0	1363	3	AAY90366	Aay90366 Human Flt
3	7211	100.0	1363	3	AAY70747	Aay70747 Human tyr
4	7211	100.0	1363	3	AAB29047	Aab29047 Human Flt
5	7211	100.0	1363	4	AAB37604	Aab37604 Human Flt
6	7211	100.0	1363	5	ABG32044	Abg32044 Human Flt
7	7211	100.0	1363	6	ABU04297	Abu04297 Human exp
8	7211	100.0	1363	6	ABU04284	Abu04284 Human exp
9	7211	100.0	1363	6	ABU04282	Abu04282 Human exp
10	7211	100.0	1363	6	ABU04295	Abu04295 Human exp
11	7167	99.4	1363	7	ADC64992	Adc64992 Human VEG
12	6852	95.0	1298	2	AAR85937	Aar85937 Protein t
13	6852	95.0	1298	2	AAR90528	Aar90528 FLT4 rece
14	6852	95.0	1298	2	ADP90836	Adp90836 Human fms
15	6852	95.0	1298	3	AAY90365	Aay90365 Human Flt
16	6852	95.0	1298	3	AAY70746	Aay70746 Human tyr
17	6852	95.0	1298	5	ABG32043	Abg32043 Human Flt
18	6852	95.0	1298	6	ABU04292	Abu04292 Human exp
19	6852	95.0	1298	6	ABU04307	Abu04307 Human exp
20	6852	95.0	1298	6	ABU04296	Abu04296 Human exp
21	6852	95.0	1298	6	ABU04274	Abu04274 Human exp
22	6852	95.0	1298	6	ABU04294	Abu04294 Human exp
23	6852	95.0	1298	6	ABU04293	Abu04293 Human exp
24	6852	95.0	1298	7	ADD08956	Add08956 Human VEG
25	6852	95.0	1298	7	ADF45098	Adf45098 Human kin
26	6852	95.0	1304	6	ABU04279	Abu04279 Human exp
27	6808	94.4	1298	4	AAY97785	Aay97785 Mouse Flt
28	6808	94.4	1298	4	AAY97575	Aay97575 Human Flt
29	6808	94.4	1298	6	ABU07853	Abu07853 Human vas
30	6808	94.4	1298	6	ABU04298	Abu04298 Human exp
31	6808	94.4	1298	6	ABU04304	Abu04304 Human exp
32	6808	94.4	1298	6	ABU04277	Abu04277 Human exp
33	6808	94.4	1298	7	ADN95352	Adn95352 Human BEC
34	6808	94.4	1298	8	ADQ91191	Adq91191 Human vas
35	6808	94.4	1298	8	ADR05211	Adr05211 Human fms
36	6791	94.2	1298	3	AAB30542	Aab30542 Amino aci
37	6791	94.2	1298	6	ABU04283	Abu04283 Human exp
38	6320	87.6	1363	4	AAB37607	Aab37607 Human pro
39	6320	87.6	1363	6	ABU04285	Abu04285 Human exp
40	2762	38.3	1356	4	AAB62475	Aab62475 Human VEG
41	2762	38.3	1356	4	AAY97576	Aay97576 Human Flk
42	2762	38.3	1356	6	ABR40196	Abr40196 Human vas
43	2762	38.3	1356	7	ADD08954	Add08954 Human VEG
44	2762	38.3	1356	7	ABM79007	Abm79007 Human VEG
45	2762	38.3	1356	7	ADF45097	Adf45097 Human kin

## RESULT 2

AAY90366

ID AAY90366 standard; protein; 1363 AA.

XX

AC AAY90366;

XX

DT 15-JAN-2001 (first entry)

XX

DE Human Flt4 receptor tyrosine kinase long form protein sequence.

XX

KW Human; Flt4 receptor tyrosine kinase; antibody; extracellular domain;

KW lymphatic vessel detection; lymphatic tissue; lymph node tissue;

KW endothelial venule; diagnosis; lymphoma; long form.

XX  
 OS Homo sapiens.  
 XX  
 PN US6107046-A.  
 XX  
 PD 22-AUG-2000.  
 XX  
 PF 28-JUL-1997; 97US-00901710.  
 XX  
 PR 09-OCT-1992; 92US-00959951.  
 PR 09-JUN-1994; 94US-00257754.  
 PR 14-NOV-1994; 94US-00340011.  
 XX  
 PA (ORIN ) ORION CORP.  
 PA (LUDW-) LUDWIG INST CANCER RES.  
 XX  
 PI Alitalo K, Aprelikova O, Armstrong E, Korhonen J, Kaipainen A;  
 PI Matikainen M, Pajusola K;  
 XX  
 DR WPI; 2000-571323/53.  
 DR N-PSDB; AAA37816.  
 XX  
 PT Antibody to extracellular domain of or to an epitope unique to a  
 PT vertebrate Flt4 receptor tyrosine kinase protein useful for diagnosing  
 PT lymphoma and imaging lymphatic vessels or high endothelial venules in  
 PT tissue.  
 XX  
 PS Claim 21; Col 55-66; 66pp; English.  
 XX  
 CC This sequence represents the human Flt4 receptor tyrosine kinase long  
 CC form protein. The invention relates to an antibody (I) specific to the  
 CC extracellular domain of or to an epitope unique to a vertebrate Flt4  
 CC receptor tyrosine kinase protein (II). A composition comprising (I) is  
 CC useful for detecting lymphatic vessels, lymphatic tissue comprising lymph  
 CC node tissue or high endothelial venules in an organism preferably mammal  
 CC especially human. The method comprises administering the composition and  
 CC detecting (I) bound to lymphatic vessels, lymphatic tissue or high  
 CC endothelial venules. (I) is also useful for screening a biological sample  
 CC for the presence of (II) or diagnosing a disease state. The diagnosing  
 CC method of the disease state preferably lymphoma comprises obtaining a  
 CC tissue sample on a vertebrate organism suspected of being in a diseased  
 CC state characterised by in Flt4 expression in lymphatic cells or high  
 CC endothelial venules and screening the diseased state utilising (I). (I)  
 CC is also useful for imaging lymphatic vessels or high endothelial venules  
 CC in a tissue by contacting the tissue with (I) and imaging the vessels by  
 CC detecting (I) bound to the tissues  
 XX  
 SQ Sequence 1363 AA;

Query Match 100.0%; Score 7211; DB 3; Length 1363;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1363; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

# RESULT 12

AAR85937

ID AAR85937 standard; protein; 1298 AA.

XX

AC AAR85937;

XX

DT 14-FEB-1996 (first entry)

XX

DE Protein tyrosine-kinase SAL-S1.

XX

KW Protein tyrosine-kinase; SAL-S1; cell growth; differentiation.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Peptide 1. .24

FT /label= Sig\_peptide

FT Domain 25. .775  
 FT /label= Extracellular\_domain  
 FT Domain 776. .800  
 FT /label= Transmembrane\_domain  
 FT Domain 801. .1298  
 FT /label= Cytoplasmic\_tyrosine\_kinase\_domain  
 XX  
 PN WO9527061-A1.  
 XX  
 PD 12-OCT-1995.  
 XX  
 PF 04-APR-1995; 95WO-US004228.  
 XX  
 PR 04-APR-1994; 94US-00222616.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Bennett BD, Goeddel D, Lee JM, Matthews W, Tsai SP, Wood WI;  
 XX  
 DR WPI; 1995-366160/47.  
 DR N-PSDB; AAT03090.  
 XX  
 PT Agonist antibodies which activate specific protein tyrosine kinase(s) -  
 PT also activate chimeric proteins of kinase extracellular domain and Ig  
 PT constant domain, useful for studying, and therapeutic modulation of, cell  
 PT growth and differentiation.  
 XX  
 PS Disclosure; Fig 15A-F; 125pp; English.  
 XX  
 CC DNA probes based on protein tyrosine-kinase (pTK) sequences were used to  
 CC screen cDNA libraries to identify novel pTK genes. The SAL-S1 gene was  
 CC isolated from several megakaryocytic cell line libraries. The gene (see  
 CC AAT03090) encodes a protein (AAR85937) showing homology to FLT/FLK family  
 CC pTKs. SAL-S1 can be used to target proteins in drug design, as an  
 CC (ant)agonist of other pTKs, to screen pTK ligands or to modulate  
 CC megakaryocyte/platelet adhesion  
 XX  
 SQ Sequence 1298 AA;

Query Match 95.0%; Score 6852; DB 2; Length 1298;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1297; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

#### Issued Patents:

#### SUMMARIES

Result No.	Score	%		DB	ID	Description
		Query Match	Length			
1	7211	100.0	1363	1	US-08-340-011-4	Sequence 4, Appli
2	7211	100.0	1363	3	US-08-901-710-4	Sequence 4, Appli
3	7211	100.0	1363	4	US-09-375-248-2	Sequence 2, Appli
4	7211	100.0	1363	4	US-09-169-079-4	Sequence 4, Appli
5	7157	99.3	1363	2	US-08-874-678-32	Sequence 32, Appl
6	7157	99.3	1363	3	US-08-643-839-32	Sequence 32, Appl
7	7157	99.3	1363	3	US-09-348-886-32	Sequence 32, Appl
8	6852	95.0	1298	1	US-08-222-616-33	Sequence 33, Appl
9	6852	95.0	1298	1	US-08-340-011-2	Sequence 2, Appli
10	6852	95.0	1298	3	US-08-901-710-2	Sequence 2, Appli
11	6852	95.0	1298	3	US-08-446-648-33	Sequence 33, Appl
12	6852	95.0	1298	4	US-09-982-610-33	Sequence 33, Appl
13	6852	95.0	1298	4	US-09-169-079-2	Sequence 2, Appli
14	6852	95.0	1298	5	PCT-US95-04228-33	Sequence 33, Appl
15	6797.5	94.3	1368	2	US-08-874-678-34	Sequence 34, Appl
16	6797.5	94.3	1368	3	US-08-643-839-34	Sequence 34, Appl
17	6797.5	94.3	1368	3	US-09-348-886-34	Sequence 34, Appl
18	6320	87.6	1363	4	US-09-375-248-19	Sequence 19, Appl
19	6005.5	83.3	1362	2	US-08-874-678-33	Sequence 33, Appl
20	6005.5	83.3	1362	3	US-08-643-839-33	Sequence 33, Appl

21	6005.5	83.3	1362	3	US-09-348-886-33	Sequence 33, Appl
22	4135	57.3	777	2	US-08-874-678-3	Sequence 3, Appli
23	4135	57.3	777	3	US-08-643-839-3	Sequence 3, Appli
24	4135	57.3	777	3	US-09-348-886-3	Sequence 3, Appli
25	2762	38.3	1356	4	US-09-949-016-6198	Sequence 6198, Ap
26	2762	38.3	1456	4	US-09-949-016-9853	Sequence 9853, Ap
27	2759	38.3	1356	3	US-09-098-707A-2	Sequence 2, Appli
28	2759	38.3	1356	3	US-09-483-539-2	Sequence 2, Appli
29	2753	38.2	1356	1	US-08-810-116-8	Sequence 8, Appli
30	2753	38.2	1356	2	US-07-930-548A-8	Sequence 8, Appli
31	2682	37.2	1367	2	US-08-443-861-2	Sequence 2, Appli
32	2682	37.2	1367	3	US-08-193-829B-2	Sequence 2, Appli
33	2665	37.0	1367	1	US-07-813-593-4	Sequence 4, Appli
34	2665	37.0	1367	1	US-07-977-451-6	Sequence 6, Appli
35	2665	37.0	1367	1	US-07-946-507-4	Sequence 4, Appli
36	2665	37.0	1367	1	US-08-252-517-6	Sequence 6, Appli
37	2665	37.0	1367	1	US-07-906-397A-6	Sequence 6, Appli

# RESULT 3

US-09-375-248-2

; Sequence 2, Application US/09375248  
; Patent No. 6764820  
; GENERAL INFORMATION:  
; APPLICANT: Ferrell, Robert E.  
; APPLICANT: Alitalo, Kari  
; APPLICANT: Finegold, David N.  
; APPLICANT: Karkkainen, Marika  
; TITLE OF INVENTION: SCREENING AND THERAPY FOR LYMPHATIC DISORDERS INVOLVING  
; TITLE OF INVENTION: THE FLT4 RECEPTOR TYROSINE KINASE (VEGFR-3)  
; FILE REFERENCE: 28967/35255A  
; CURRENT APPLICATION NUMBER: US/09/375,248  
; CURRENT FILING DATE: 1999-08-16  
; EARLIER APPLICATION NUMBER: PCT/US99/06133  
; EARLIER FILING DATE: 1999-03-26  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 1363  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-375-248-2

Query Match 100.0%; Score 7211; DB 4; Length 1363;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1363; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

# RESULT 5

US-08-874-678-32

; Sequence 32, Application US/08874678  
; Patent No. 5952199  
; GENERAL INFORMATION:  
; APPLICANT: Davis-Smyth, Terri L.  
; APPLICANT: Chen, Helen H.  
; APPLICANT: Presta, Leonard  
; APPLICANT: Ferrara, Napoleone  
; TITLE OF INVENTION: NOVEL INHIBITORS OF VASCULAR ENDOTHELIAL GROWTH FACTOR  
; TITLE OF INVENTION: ACTIVITY, THEIR USES AND PROCESSES FOR THEIR PRODUCTION  
; NUMBER OF SEQUENCES: 48  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert  
; STREET: Four Embarcadero Center, Suite 3400  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: United States  
; ZIP: 94111-4187  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS

5-7-96

; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/874,678  
; FILING DATE: HEREWITH  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/643,839  
; FILING DATE: 07-MAY-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Dreger, Walter H.  
; REGISTRATION NUMBER: 24,190  
; REFERENCE/DOCKET NUMBER: A-63291-1/WH  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 781-1989  
; TELEFAX: (415) 398-3249  
; TELEX: 910 277299  
; INFORMATION FOR SEQ ID NO: 32:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1363 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: unknown  
; TOPOLOGY: unknown  
; MOLECULE TYPE: protein  
US-08-874-678-32

Query Match 99.3%; Score 7157; DB 2; Length 1363;  
Best Local Similarity 99.3%; Pred. No. 0;  
Matches 1354; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

RESULT 8

US-08-222-616-33

; Sequence 33, Application US/08222616  
; Patent No. 5635177  
; GENERAL INFORMATION:  
; APPLICANT: Bennett, Brian D.  
; APPLICANT: Goeddel, David  
; APPLICANT: Lee, James M.  
; APPLICANT: Matthews, William  
; APPLICANT: Tsai, Siao Ping  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: PROTEIN TYROSINE KINASE AGONIST  
; TITLE OF INVENTION: ANTIBODIES  
; NUMBER OF SEQUENCES: 42  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 460 Point San Bruno Blvd  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: patin (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/222,616  
; FILING DATE: 4-APR-1994  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US93/00586  
; FILING DATE: 22-JAN-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/826935  
; FILING DATE: 22-JAN-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lee, Wendy M.  
; REGISTRATION NUMBER:  
; REFERENCE/DOCKET NUMBER: 821P2  
; TELECOMMUNICATION INFORMATION:



; TELEPHONE: 415/225-1994  
; TELEFAX: 415/952-9881  
; TELEX: 910/371-7168  
; INFORMATION FOR SEQ ID NO: 33:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1298 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
US-08-222-616-33

Query Match 95.0%; Score 6852; DB 1; Length 1298;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1297; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 11

US-08-446-648-33

; Sequence 33, Application US/08446648  
; Patent No. 6331302

; GENERAL INFORMATION:

; APPLICANT: Genentech, Inc.  
; APPLICANT: Bennett, Brian D.  
; APPLICANT: Goeddel, David  
; APPLICANT: Lee, James M.  
; APPLICANT: Matthews, William  
; APPLICANT: Tsai, Siao Ping  
; APPLICANT: Wood, William I.

; TITLE OF INVENTION: PROTEIN TYROSINE KINASE AGONIST ANTIBODIES

; NUMBER OF SEQUENCES: 45

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Genentech, Inc.  
; STREET: 460 Point San Bruno Blvd  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatin (Genentech)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/446,648

; FILING DATE:

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/222616

; FILING DATE: 04-APR-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: Lee, Wendy M.  
; REGISTRATION NUMBER: 40,378  
; REFERENCE/DOCKET NUMBER: P0821P3PCT

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415/225-1994  
; TELEFAX: 415/952-9881  
; TELEX: 910/371-7168

; INFORMATION FOR SEQ ID NO: 33:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1298 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear

US-08-446-648-33

Query Match 95.0%; Score 6852; DB 3; Length 1298;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1297; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

PGPUBS:

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	7211	100.0	1363	10	US-09-375-248-2	Sequence 2, Appli
2	7211	100.0	1363	11	US-09-765-534B-4	Sequence 4, Appli
3	7211	100.0	1363	15	US-10-661-740-2	Sequence 2, Appli
4	7211	100.0	1363	16	US-10-774-802-4	Sequence 4, Appli
5	7211	100.0	1363	16	US-10-473-127-948	Sequence 948, App
6	7211	100.0	1363	16	US-10-473-127-950	Sequence 950, App
7	7211	100.0	1363	16	US-10-473-127-961	Sequence 961, App
8	7211	100.0	1363	16	US-10-473-127-963	Sequence 963, App
9	7167	99.4	1363	14	US-10-081-126-2	Sequence 2, Appli
10	7157	99.3	1363	14	US-10-105-901-32	Sequence 32, Appl
11	6852	95.0	1298	9	US-09-982-610-33	Sequence 33, Appl
12	6852	95.0	1298	11	US-09-765-534B-2	Sequence 2, Appli
13	6852	95.0	1298	14	US-10-262-538-32	Sequence 32, Appl
14	6852	95.0	1298	15	US-10-394-322A-67	Sequence 67, Appl
15	6852	95.0	1298	16	US-10-774-802-2	Sequence 2, Appli
16	6852	95.0	1298	16	US-10-669-176-32	Sequence 32, Appl
17	6852	95.0	1298	16	US-10-473-127-940	Sequence 940, App
18	6852	95.0	1298	16	US-10-473-127-958	Sequence 958, App
19	6852	95.0	1298	16	US-10-473-127-959	Sequence 959, App
20	6852	95.0	1298	16	US-10-473-127-960	Sequence 960, App
21	6852	95.0	1298	16	US-10-473-127-962	Sequence 962, App
22	6852	95.0	1298	16	US-10-473-127-973	Sequence 973, App
23	6852	95.0	1304	16	US-10-473-127-945	Sequence 945, App
24	6808	94.4	1298	15	US-10-165-193A-12	Sequence 12, Appl
25	6808	94.4	1298	16	US-10-326-048-4	Sequence 4, Appli
26	6808	94.4	1298	16	US-10-473-127-943	Sequence 943, App
27	6808	94.4	1298	16	US-10-473-127-964	Sequence 964, App
28	6808	94.4	1298	16	US-10-473-127-970	Sequence 970, App
29	6808	94.4	1298	17	US-10-781-581-222	Sequence 222, App
30	6797.5	94.3	1368	14	US-10-105-901-34	Sequence 34, Appl
31	6791	94.2	1298	16	US-10-473-127-949	Sequence 949, App
32	6320	87.6	1363	10	US-09-375-248-19	Sequence 19, Appl
33	6320	87.6	1363	15	US-10-661-740-19	Sequence 19, Appl
34	6320	87.6	1363	16	US-10-473-127-951	Sequence 951, App
35	6005.5	83.3	1362	14	US-10-105-901-33	Sequence 33, Appl
36	4135	57.3	777	14	US-10-105-901-3	Sequence 3, Appli
37	2762	38.3	1356	14	US-10-090-183-2	Sequence 2, Appli
38	2762	38.3	1356	15	US-10-394-322A-66	Sequence 66, Appl
39	2762	38.3	1356	15	US-10-440-464-129	Sequence 129, App
40	2762	38.3	1356	16	US-10-783-528-61	Sequence 61, Appl
41	2762	38.3	1356	17	US-10-872-198-115	Sequence 115, App
42	2762	38.3	1356	17	US-10-741-600-1469	Sequence 1469, Ap
43	2762	38.3	1356	17	US-10-741-600-1471	Sequence 1471, Ap
44	2762	38.3	1356	17	US-10-926-806-10	Sequence 10, Appl
45	2762	38.3	1356	20	US-11-021-951-115	Sequence 115, App

## RESULT 2

US-09-765-534B-4

; Sequence 4, Application US/09765534B

; Publication No. US20040037820A1

; GENERAL INFORMATION:

; APPLICANT: Alitalo, Kari

; APPLICANT: Kaipainen, Arja

; APPLICANT: Valtola, Reija

; APPLICANT: Jussila, Lotta

; TITLE OF INVENTION: Flt4 (VEGFR-3) as a Target for Tumor Imaging and Anti-Tumor Therapy

; FILE REFERENCE: 28113/34891

; CURRENT APPLICATION NUMBER: US/09/765,534B

; CURRENT FILING DATE: 2001-01-19

; PRIOR APPLICATION NUMBER: 08/901,710

; PRIOR FILING DATE: 1997-07-28

; PRIOR APPLICATION NUMBER: 08/340,011

; PRIOR FILING DATE: 1994-11-14

; PRIOR APPLICATION NUMBER: 08/257,754

; PRIOR FILING DATE: 1994-07-09  
 ; PRIOR APPLICATION NUMBER: 07/959,951  
 ; PRIOR FILING DATE: 1992-10-09  
 ; NUMBER OF SEQ ID NOS: 22  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 4  
 ; LENGTH: 1363  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-765-534B-4

Query Match 100.0%; Score 7211; DB 11; Length 1363;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1363; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

# SUMMARIES

Result No.	Query		DB	ID	Description
	Score	Match Length			
1	6852	95.0 1298	2	A48999	protein-tyrosine k
2	6320	87.6 1363	2	I58375	protein-tyrosine k
3	4919.5	68.2 1379	2	JC4954	vascular endotheli
4	2804	38.9 1348	2	S51656	vascular endotheli
5	2753	38.2 1356	2	JC1402	protein-tyrosine k
6	2669	37.0 1367	2	A41228	protein-tyrosine k
7	2469	34.2 1333	2	I78875	receptor tyrosine
8	2463	34.2 1338	2	S09982	protein-tyrosine k
9	2444.5	33.9 1336	2	I60598	Fit-1 tyrosine kin
10	2437.5	33.8 1330	2	S49010	embryonic receptor
11	1283.5	17.8 367	2	B56598	endothelial kinase
12	1163.5	16.1 1089	1	PFHUGA	platelet-derived g
13	1151	16.0 1088	1	PFRTGA	platelet-derived g
14	1125	15.6 1089	1	S33727	platelet-derived g
15	1122.5	15.6 1087	2	I51552	platelet-derived g
16	1084	15.0 1106	1	PFHUGB	platelet-derived g
17	1052.5	14.6 1098	1	PFMSRB	platelet-derived g
18	1051	14.6 975	2	T30816	macrophage colony-
19	1044	14.5 978	1	A49814	protein-tyrosine k
20	1042.5	14.5 976	1	TVHUKT	protein-tyrosine k
21	1033.5	14.3 975	1	TVMSKT	protein-tyrosine k
22	1024	14.2 977	2	I45877	protein-tyrosine k
23	1021.5	14.2 960	1	JN0677	protein-tyrosine k
24	1018	14.1 954	2	I51703	c-kit-related kina
25	1012	14.0 1048	2	T30815	platelet-derived g
26	967	13.4 980	1	TVCTMD	macrophage colony-
27	956	13.3 941	1	TVMVMD	protein-tyrosine k
28	954.5	13.2 972	1	TVHUMD	macrophage colony-
29	954.5	13.2 992	2	A39931	protein-tyrosine k
30	951	13.2 1000	2	S18827	Flt3 protein - mou
31	949	13.2 978	2	S16385	macrophage colony-
32	930.5	12.9 976	1	TVMSMD	macrophage colony-
33	896	12.4 806	2	A35963	protein-tyrosine k
34	895.5	12.4 687	2	A49636	soluble vascular e
35	893.5	12.4 993	2	A36873	protein-tyrosine k
36	886.5	12.3 797	2	S38579	fibroblast growth
37	873	12.1 790	1	FOMVHZ	gag-kit polyprotei
38	869	12.1 822	1	TVHUFG	fibroblast growth
39	866	12.0 822	1	TVMSFG	fibroblast growth
40	865	12.0 814	1	A39752	fibroblast growth
41	863.5	12.0 822	2	B54846	fibroblast growth
42	862	12.0 822	2	S29840	fibroblast growth
43	862	12.0 832	2	JH0393	fibroblast growth
44	861.5	11.9 800	1	TVHU2F	fibroblast growth
45	861.5	11.9 800	2	A48991	heparin-binding gr

RESULT 1  
 A48999

protein-tyrosine kinase (EC 2.7.1.112) flt4 precursor - human  
N;Alternate names: class III receptor tyrosine kinase FLT4; fms-like tyrosine kinase 4  
C;Species: Homo sapiens (man)  
C;Date: 21-Jan-1994 #sequence\_revision 18-Nov-1994 #text\_change 09-Jul-2004  
C;Accession: A48999; A44930; G02316; S36130; A42010  
R;Pajusola, K.; Aprelikova, O.; Korhonen, J.; Kaipainen, A.; Pertovaara, L.; Alitalo, R.; Alitalo, K.  
Cancer Res. 52, 5738-5743, 1992  
A;Title: FLT4 receptor tyrosine kinase contains seven immunoglobulin-like loops and is expressed in multiple human tissues and cell lines.  
A;Reference number: A48999; MUID:93007958; PMID:1327515  
A;Accession: A48999  
A;Status: preliminary; not compared with conceptual translation  
A;Molecule type: mRNA  
A;Residues: 1-1298 <PAJ>  
A;Cross-references: UNIPROT:P35916; PIDN:AAB23636.1; PID:g257352  
A;Experimental source: HEL erythroleukemia cells  
A;Note: sequence extracted from NCBI backbone (NCBIP:115335)  
R;Aprelikova, O.; Pajusola, K.; Partanen, J.; Armstrong, E.; Alitalo, R.; Bailey, S.K.; McMahon, J.; Wasmuth, J.; Huebner, K.; Alitalo, K.  
Cancer Res. 52, 746-748, 1992  
A;Title: FLT4, a novel class III receptor tyrosine kinase in chromosome 5q33-qter.  
A;Reference number: A44930; MUID:92119639; PMID:1310071  
A;Accession: A44930  
A;Status: preliminary; not compared with conceptual translation  
A;Molecule type: mRNA  
A;Residues: 761-1190 <APR>  
A;Cross-references: GB:X68203; NID:g31433  
A;Note: sequence extracted from NCBI backbone (NCBIP:78155)  
R;Wood, W.I.  
submitted to the EMBL Data Library, December 1995  
A;Reference number: H01039  
A;Accession: G02316  
A;Status: translated from GB/EMBL/DDBJ  
A;Molecule type: mRNA  
A;Residues: 1-1298 <WOO>  
A;Cross-references: EMBL:U43143; NID:g1150990; PIDN:AAA85215.1; PID:g1150991  
R;Galland, F.  
submitted to the EMBL Data Library, December 1992  
A;Reference number: S36130  
A;Accession: S36130  
A;Molecule type: mRNA  
A;Residues: 1-23, 'D', 25-744, 'P', 746-751, 'RP', 754-889, 'Q', 891-1127, 'V', 1129-1145, 'H', 1147-1163, 'D', 1165-1298 <GAL1>  
A;Cross-references: EMBL:X69878; NID:g297049; PIDN:CAA49505.1; PID:g297050  
R;Galland, F.; Karamysheva, A.; Mattei, M.G.; Rosnet, O.; Marchetto, S.; Birnbaum, D.  
Genomics 13, 475-478, 1992  
A;Title: Chromosomal localization of FLT4, a novel receptor-type tyrosine kinase gene.  
A;Reference number: A42010; MUID:92307693; PMID:1319394  
A;Accession: A42010  
A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual translation  
A;Molecule type: mRNA  
A;Residues: 776-889, 'Q', 891-1127, 'V', 1129-1145, 'H', 1147-1163, 'D', 1165-1200 <GAL2>  
C;Genetics:  
A;Gene: GDB:FLT4  
A;Cross-references: GDB:128732; OMIM:136352  
A;Map position: 5q34-5q35  
C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homology  
C;Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; transmembrane protein; tyrosine-specific protein kinase  
F;1-23/Domain: signal sequence #status predicted <SIG>  
F;24-1298/Product: protein-tyrosine kinase FLT4 #status predicted <MAT>  
F;843-1176/Domain: protein kinase homology <KIN>  
F;851-859/Region: protein kinase ATP-binding motif

Query Match 95.0%; Score 6852; DB 2; Length 1298;  
Best Local Similarity 100.0%; Pred. No. 2.3e-301;  
Matches 1297; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MQRGAALCLRLWLCGLLDGLVSGYSMTPTLNITEESHVIDTGDSLSISCRGQHLEWA	60
Db	1	MQRGAALCLRLWLCGLLDGLVSGYSMTPTLNITEESHVIDTGDSLSISCRGQHLEWA	60
Qy	61	WPGAQEAPATGDKDSEDGTVVRDCEGTDARPYCKVLLLHEVHANDTGSYVCYYKYIKARI	120
Db	61	WPGAQEAPATGDKDSEDGTVVRDCEGTDARPYCKVLLLHEVHANDTGSYVCYYKYIKARI	120
Qy	121	EGTTAASSYVFVRDFEQPFINKPDTLLVNRKDAMWVPCLVSIPLNVTLSQSSSLWPDG	180
Db	121	EGTTAASSYVFVRDFEQPFINKPDTLLVNRKDAMWVPCLVSIPLNVTLSQSSSLWPDG	180
Qy	181	QEVVWDDRRGMLVSTPLLHDALYLQCETTWGDQDFLSNPFLVHITGNELYDIQLLPRKSL	240
Db	181	QEVVWDDRRGMLVSTPLLHDALYLQCETTWGDQDFLSNPFLVHITGNELYDIQLLPRKSL	240
Qy	241	ELLVGEKLVLNCTVWAEFNSGVTFDWDYPGKQAERGKWVPERRSQQTHTELSSILTIHNV	300
Db	241	ELLVGEKLVLNCTVWAEFNSGVTFDWDYPGKQAERGKWVPERRSQQTHTELSSILTIHNV	300
Qy	301	SQHDLSGSYVCKANNGIQRFRESTEVIHNPFIISVEWLKGPILEATAGDELVKLPVKLAA	360
Db	301	SQHDLSGSYVCKANNGIQRFRESTEVIHNPFIISVEWLKGPILEATAGDELVKLPVKLAA	360
Qy	361	YPPPEFQWYKDGKALSGRHSPhALVLKEVTEASTGTYTLALWNSAAGLRRNISLELVNV	420
Db	361	YPPPEFQWYKDGKALSGRHSPhALVLKEVTEASTGTYTLALWNSAAGLRRNISLELVNV	420
Qy	421	PPQIHEKEASSPSIYSRHSRQALTCTAYGVPLPLSIQWHWRPWTCKMFAQSLRRRQQQ	480
Db	421	PPQIHEKEASSPSIYSRHSRQALTCTAYGVPLPLSIQWHWRPWTCKMFAQSLRRRQQQ	480
Qy	481	DLMPQCRDRAVTTQDAVNPIESLDTWTEFVEGKNKTVSKLVIQANVSAMYKCVVSNKV	540
Db	481	DLMPQCRDRAVTTQDAVNPIESLDTWTEFVEGKNKTVSKLVIQANVSAMYKCVVSNKV	540
Qy	541	GQDERLIYFYVTTIPDGFTIESKPSHEELLEGQPVLLSCQADSYKYEHLRWYRLNLSLTHD	600
Db	541	GQDERLIYFYVTTIPDGFTIESKPSHEELLEGQPVLLSCQADSYKYEHLRWYRLNLSLTHD	600
Qy	601	AHGNPLLLDCKNVHLFATPLAASLEEVPAGARHATLSLSIPRVAPEHEGHYVCEVQDRRS	660
Db	601	AHGNPLLLDCKNVHLFATPLAASLEEVPAGARHATLSLSIPRVAPEHEGHYVCEVQDRRS	660
Qy	661	HDKHCHKYLSVQALEAPRLTQNLTDLLVNVSDSLEMQCLVAGAHAPSIVWYKDERLLEE	720
Db	661	HDKHCHKYLSVQALEAPRLTQNLTDLLVNVSDSLEMQCLVAGAHAPSIVWYKDERLLEE	720
Qy	721	KSGVDLADSNQKLSIQRVREEDAGRYLCSVCNAKGCNVSSASVAVEGSEDKGSMEIVILV	780
Db	721	KSGVDLADSNQKLSIQRVREEDAGRYLCSVCNAKGCNVSSASVAVEGSEDKGSMEIVILV	780
Qy	781	GTGVIAVFFWVLLLLIFCNMRRPAHADIKTGYSIIMDPGEVPLEEQCEYLSYDASQWEF	840
Db	781	GTGVIAVFFWVLLLLIFCNMRRPAHADIKTGYSIIMDPGEVPLEEQCEYLSYDASQWEF	840
Qy	841	PRERLHLGRVLGYGAFGKVVEASAFGIHKGSSCDTVAVKMLKEGATASEHRALMSELKIL	900
Db	841	PRERLHLGRVLGYGAFGKVVEASAFGIHKGSSCDTVAVKMLKEGATASEHRALMSELKIL	900
Qy	901	IHIGNHLNVVNLLGACTKPQGFLMVIVEFCKYGNLSNFLRAKRDAFSPCAEKSPEQRGRF	960
Db	901	IHIGNHLNVVNLLGACTKPQGFLMVIVEFCKYGNLSNFLRAKRDAFSPCAEKSPEQRGRF	960
Qy	961	RAMVELARLDRRRPGSSDRVLFARFSKTEGGARRASPDQEAEDLWLSPLTMEDLVCYSFQ	1020
Db	961	RAMVELARLDRRRPGSSDRVLFARFSKTEGGARRASPDQEAEDLWLSPLTMEDLVCYSFQ	1020
Qy	1021	VARGMEFLASRKCIHRDLAARNILLSES DVVKICDFGLARDIYKDPDYVRKGSARLPLKW	1080
Db	1021	VARGMEFLASRKCIHRDLAARNILLSES DVVKICDFGLARDIYKDPDYVRKGSARLPLKW	1080

Qy 1081 MAPESIFDKVYTTQSDVWSFGVLLWEIFSLGASPYPGVQINEEFCQRLRDGTRMRAPELA 1140  
 |||||  
 Db 1081 MAPESIFDKVYTTQSDVWSFGVLLWEIFSLGASPYPGVQINEEFCQRLRDGTRMRAPELA 1140  
 |||||  
 Qy 1141 TPAIRRIMLNCWSGDPKARPAFSELVEILGDLQGRGLQEEEEVCMAPRSSQSSEEGSFS 1200  
 |||||  
 Db 1141 TPAIRRIMLNCWSGDPKARPAFSELVEILGDLQGRGLQEEEEVCMAPRSSQSSEEGSFS 1200  
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 Qy 1201 QVSTMALHIAQADAEDSPPSLQRHSLAARYYNWVSFPGCLARGAETRGSRRMKTFFEEFPM 1260  
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 Db 1201 QVSTMALHIAQADAEDSPPSLQRHSLAARYYNWVSFPGCLARGAETRGSRRMKTFFEEFPM 1260  
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 Qy 1261 TPTTYKGSVDNQTDSGMVLASEEFEQIESRHRQESGF 1297  
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 Db 1261 TPTTYKGSVDNQTDSGMVLASEEFEQIESRHRQESGF 1297  
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## RESULT 2

I58375

protein-tyrosine kinase (EC 2.7.1.112) flt4 - mouse

C;Species: Mus musculus (house mouse)

C;Date: 26-Jul-1996 #sequence\_revision 26-Jul-1996 #text\_change 16-Aug-2004

C;Accession: I58375; B42010

R;Finnerty, H.; Kelleher, K.; Morris, G.E.; Bean, K.; Merberg, D.M.; Kriz, R.; Morris, J.C.; Sookdeo, H.; Turner, K.J.; Wood, C.R.

Oncogene 8, 2293-2298, 1993

A;Title: Molecular cloning of murine FLT and FLT4.

A;Reference number: I58375; MUID:93330572; PMID:8393164

A;Accession: I58375

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-1363 <RES>

A;Cross-references: UNIPROT:P35917; GB:L07296; NID:g293780; PIDN:AAA40077.1; PID:g293781

R;Galland, F.; Karamysheva, A.; Mattei, M.G.; Rosnet, O.; Marchetto, S.; Birnbaum, D.

Genomics 13, 475-478, 1992

A;Title: Chromosomal localization of FLT4, a novel receptor-type tyrosine kinase gene.

A;Reference number: A42010; MUID:92307693; PMID:1319394

A;Accession: B42010

A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual translation

A;Molecule type: DNA

A;Residues: 1033-1072 <GAL>

C;Genetics:

A;Gene: FTL4

C;Superfamily: protein kinase homology

C;Keywords: ATP; phosphotransferase; tyrosine-specific protein kinase

F;843-1176/Domain: protein kinase homology <KIN>

F;851-859/Region: protein kinase ATP-binding motif

Query Match 87.6%; Score 6320; DB 2; Length 1363;  
 Best Local Similarity 87.5%; Pred. No. 2.2e-277;  
 Matches 1192; Conservative 68; Mismatches 103; Indels 0; Gaps 0;

Qy 1 MQRGAALCLRLWLCGLLDGLVSGYSMTPTPLNITEESHVIDTGDLSISICRGQHPLEWA 60  
 || |||||  
 Db 1 MQPGAALNRLWLCGLLQGLANGYSMTPTPLNITEDSYVIDTGDLSISICRGQHPLEWT 60  
 || |||||  
 Qy 61 WPGAQEAPATGDKDSED TG VVRDCEGTDARPYCKVLLLEHVHANDTGSYVCYYKYIKARI 120  
 ||||| || ||||| || |||||: ||||| : |||||  
 Db 61 WPGAQEVLTGDKDSEDTRVVDCEGTEARPYCKVLLLAQTHANNTGSYHCYYKYIKARI 120  
 ||||| || ||||| || |||||: ||||| : |||||  
 Qy 121 EGTTAASSYVVRDFEQPFINKPDTLLVNRKDAMWVPCLVSIPLNITLRSQSSVLWPDG 180  
 |||||: |||||: |||||: |||||: |||||: |||||  
 Db 121 EGTTAASTYVVRDFKHPFINKPDTLLVNRKDSMWVPCLVSIPLNITLRSQSSALHPDG 180  
 |||||: |||||: |||||: |||||: |||||: |||||  
 Qy 181 QEVVWDDRRGMLVSTPLLHDALYLQCETTWGDQDFLSNPFLVHITGNELYDIQLLPKSKL 240  
 |||: ||||| || || |||||: ||||| : |||||: |||||  
 Db 181 QEVLWDDRRGMVPTQLLRDALYLQCETTWGDQNFSLNLFVVHITGNELYDIQLYPKKSM 240  
 |||||: |||||: |||||: |||||: |||||: |||||  
 Qy 241 ELLVGEKLVLNCTVWAEFNSGVTFDWDYPGKQAERGKWVPERRSQQTHTLSSILTIHNV 300

Db	241	ELLVGEKLVLNCTVWAEFDSGVTFDWDYPGKQAEAKWVPERRSQQTHTLSSILTIHNV	300
Qy	301	SQHDLGSYVCKANNGIQRFRESTEVIVHENPFISVEWLKGPILEATAGDELVKLPVKLAA	360
Db	301	SQNDLGPYVCEANNGIQRFRESTEVIVHEKPFISVEWLKGPVLEATAGDELVKLPVKLAA	360
Qy	361	YPPPEFQWYKDGKALSGRHSHPHALVLKEVTEASTGTYTLALWNSAAGLRNNISLELVNV	420
Db	361	YPPPEFQWYKDRKAVTGRHNPHALVLKEVTEASAGVYTLALWNSAAGLRQNNISLELVNV	420
Qy	421	PPQIHEKEASSPSIYSRHSRQALTCTAYGVPLPLSIQWHWRPWPCKMFAQRS�RRRQQQ	480
Db	421	PPHIHEKEASSPSIYSRHSRQTLCTAYGVQPLSVQWHWRPWPCKTFAQRS�RRRQQR	480
Qy	481	DLMPQCRDWRAVTTQDAVNPIESLDTWTEFVEGKNKTVSKLVIQANVVSAMYKCVVSNKV	540
Db	481	DGMPQCRDWKEVTTQDAVNPIESLDSWTEFVEGKNKTVSKLVIQDANVVSAMYKCVVNVK	540
Qy	541	GQDERLIYFYVTTIPDGFTIESKPSEELLEGQPVLLSCQADSZYKYEHLRWYRLNLSLTHD	600
Db	541	GQDERLIYFYVTTIPDGFSIESEPSDPLEGQSVRLSCRADNYTYEHLRWYRLNLSLTHD	600
Qy	601	AHGNPLLLDCKNVHLFATPLAASLEEAPGARHATLSLSIPRVAPEHEGHYVCEVQDRRS	660
Db	601	AQGNPLLLDCKNVHLFATPLEANLEAEAPGARHATLSLNI PRVAPEDEGDYVCEVQDRRS	660
Qy	661	HDKHCHKYLSVQALEAPRLTQNLTDLLVNVSDSLEMQCLVAGAHAPSIVWYKDERLLEE	720
Db	661	QDKHCHKYLSVQALEAPRLTQNLTDLLVNVSDSLEMRCPVAGAHVPSIVWYKDERLLEK	720
Qy	721	KSGVDLADSNQKLSIQRVREEDAGRYLCSVCNAKGCVNSSASVAVEGSEDKGSMEIVILV	780
Db	721	ESGIDLADSNQRLSIQRVREEDAGRYLCSVCNAKGCVNSSASVAVEGSEDKGSMEIVILI	780
Qy	781	GTGVIAVFFWVLLLLIFCNMRRPAHADIKTGYSIIMDPGEVPLEEQCEYLSYDASQWEF	840
Db	781	GTGVIAVFFWVLLLLIFCNMKRPAHADIKTGYSIIMDPGEVPLEEQCEYLSYDASQWEF	840
Qy	841	PRERLHLGRVLGYGAFGKVVEASAFGIHKGSSCDTVAVKMLKEGATASEHRLMSELKIL	900
Db	841	PRERLHLGRVLGHGAFGKVVEASAFGINKGSSCDTVAVKMLKEGATASEHRLMSELKIL	900
Qy	901	IHIGNHLNVVNLGACTKPGQPLMVIVEFCKYGNLSNFLRAKRDAFSPCAEKSPEQRGRF	960
Db	901	IHIGNHLNVVNLGACTKPNGPLMVIVEFCKYGNLSNFLRVKRDFTFNPYAEKSPEQRRRF	960
Qy	961	RAMVELARLDRRRPGSSDRVLFAFBSKTEGGARRASPDQEAEDLWLSPLTMEDLVCYSFQ	1020
Db	961	RAMVEGAKADRRRPGSSDRALFTRFLMGKSARRAPLVQEAEDLWLSPLTMEDLVCYSFQ	1020
Qy	1021	VARGMEFLASRKCIHRDLAARNILLSSEDVVKICDFGLARDIYKDPDYVRKGSARLPLKW	1080
Db	1021	VARGMEFLASRKCIHRDLAARNILLSSEDIVKICDFGLARDIYKDPDYVRKGSARLPLKW	1080
Qy	1081	MAPESIFDKVYTTQSDVWSFGVLLWEIFSLGASPYPGVQINEEFCQRLRDGTRMRAPELA	1140
Db	1081	MAPESIFDKVYTTQSDVWSFGVLLWEIFSLGASPYPGVQINEEFCQRLKDGTRMRAPELA	1140
Qy	1141	TPAIRRIMLNCWSGDPKARPAFSELVEILGDLQGRGLQEEEEVCMAPRSSQSSEEGSFS	1200
Db	1141	TPAIRHIMQSCWSGDPKARPAFSDLVEILGDLQGGGWQEEEEERMAHSSQSSEEDGFM	1200
Qy	1201	QVSTMALHIAQADAEDSPPSLQRHSLAARYYNWVSFPGCLARGAETRGSSRMKTFEFFPM	1260
Db	1201	QASTTALHITEADADDSPPSMHCHSLAARYYNCVSFPGRLARGTKTPGSSRMKTFEELPM	1260
Qy	1261	TPTTYKGSVDNQTDSGMVLASEEFEQIESRHRQESGFSCKGPGQNVAVTRAHPDSQGRRR	1320
Db	1261	TPTTYKASMDNOTDSGMVLASEEFEELESRHRPEGSFSCKGPGOHMDIPRGHPDPOGRRR	1320

Qy 1321 RPERGARGGQVFYNSEYGEELSEPSEEDHCSPSARVTFFTDNSY 1363  
|| :||:|||:|||:|||:||| :|| | ||| ||| |:||  
Db 1321 RPTOGAOGGKVIFYNNEYGEVSQPCTEGDCCPSAGSTFFADSSY 1363

Query Match 38.2%; Score 2753; DB 2; Length 1356;  
Best Local Similarity 43.9%; Pred. No. 1.1e-116;  
Matches 606; Conservative 205; Mismatches 480; Indels 88; Gaps 26;

Qy	1	MQRGAALCLRLWLCIGLLDLGLVS--GYSMTPPTLNITEESHVIDTGDLSLSISCRGQHPL	58
		:   :       :   :   :   :   :   :           :	
Db	1	MESKVLVALVALWLCVETRAASVGLPSVSLDLPRLSLIQKDILTIKANTTLQITCRGQRDL	60
Qy	59	WAWPGAQEAPATGDKDSEDGTGVVRDC-EGTDARPYCKVLLLEHVHANDTGSYVCYYKYIK	117
		:   :   :   :   :       :   :   :	
Db	61	WLWPNNQSG-----SEQRVEVTECSDDL----FCKTLTIPKVIQNDTGAYKCFYR---	106
Qy	118	ARIEGTTAASSYVVRDFEQPFINKPDT-----LLVNRKDMAMWVCLVSIPLNVTL--	169
		:   :   :   :   :   :   :   :           :	
Db	107	---ETDLASVIYVYQDYRSPFIASVSDQHGVVYITENKNKTVVIPCGLSISNLNVSLCA	163
Qy	170	RSQSSVLWPDGQEVVWDDRRGMLVSTPLLHDALYLQCETTWGDQDFLSNPFLVHITGNEL	229
		:     :   :   :   :       :   :   :   :   :	
Db	164	RYPEKRFVPDGNRISWDSKKGFITPSYMISYAGMVFCFAKINDESYQSIMYIVVVVGYRI	223
Qy	230	YDIQLLPKRSLELLVGEKLVNLCTVWAEFNSGVTFDWDYPGKQAERGKWPERRSQQTH	289
		:     :                       :   :   :   :   :	
Db	224	YDVVLSPSHGIELSVGEKLVNLCTARTELVNGIDFNWEYPSKKHQHKKLVNRDLKTQSGS	283
Qy	290	ELS---SILTIHNVSOHDLGSYVCKANNGIORFRESTEVIHNPFIISVEWLKGPPILEAT	346



Db	284	EMKKFLSTLTIDGVTRSDQGLYTCAASSGLMTKKNSTFVRVHEKPFVAFSGMESLVEAT	343
Qy	347	AGDELVKLPVKLAAYPPPEFQWKDGKALSGRH---SPHALVLKEVTEASTGTYTLALWN	403
Db	344	VG-ERVRIPAKYLGYPPPEIKWKNGIPLSNHTIKAGHVLTIMEVSESDTGNVTVILT	402
Qy	404	SAAGLRRNISLELVNVPPQIHEKEASSP-SIYSRHSRQALTCTAYGVPLPLSIQWHWRP	462
Db	403	PISKEKQSHVSVLVVYVPPQIGEKSLISPVDSYQYGTQTTLCTVYAIPPPHHIHWYWL	462
Qy	463	WTPCKMFAQRSLRRRQQQDLMPQCRDWRVTTQDAVNPIESLDTWTEFVEGKNKTVSKLV	522
Db	463	EEEC---ANEPSQAVSVTNYP-CEEWSVEDFQGGNKIEVNKNQFALIEGKNKTVSTLV	518
Qy	523	IQNANVSAMYKCVVSNKVGQDERLIYFYVTTIPDGFTIESKPSEELLEGQPVLLSCQADS	582
Db	519	IQAANVSALYKCEAVNKVGRGERVISFHVTRGPE---ITLQPDMPQTEQESVSLWCTADR	575
Qy	583	YKYEHLRWYRLNLSTLHDAHGNPLLLDCKNV---HLFATPLAASLEEVAPGARHATLSL	638
Db	576	STFENLTWYKLGPPQLPIHVGEPLTPVCKNLDLTKLNLATMFSNSTNDI-----LIM	627
Qy	639	SIPRVAPEHEGHYVCEVQDRRSHDKHCHKYLSVQALEAPRLTQNLTDLLVNVSDSLEMQ	698
Db	628	ELKNASLQDQGDYVCLAQDRKTKKRHCVVRLTVLERVAPTITGNLENQTTSIGESIEVS	687
Qy	699	CLVAGAHAPSIVWYKDERLLEKSGVDLADSNQKLSIQRVREEDAGRYLCSVCNAKGCVN	758
Db	688	CTASGNPPQIMWFKDNETLVEDSGIVLKDGNRNLTIRVRKEDEGLYTCQACSVLGCAK	747
Qy	759	SSASVAVEGSEDKGSMEIVILVGTGVIIVFFWVLLLLIFCNMRRPAHADIKTYLSIIMD	818
Db	748	VEAFFIIEGAQEKTNLEIIILVGTTVIAMFFWVLLVILGTVKRANGGELKTGYLSIVMD	807
Qy	819	PGEVPLEEQCEYLSYDASQWEFPRERLHLGRVLGYGAFGKVVEASAFGIHKGSSCDTVAV	878
Db	808	PDELPLDEHCERLPYDASKWEFPRDRLNLGKPLGRGAFGEIADAFGIDKTATCRTVAV	867
Qy	879	KMLKEGATASEHRALMSELKILIHIGHNLNVNLLGACTKPGGPLMVIVEFCKYGNLSNF	938
Db	868	KMLKEGATHSEHRALMSELKILIHIGHNLNVNLLGACTKPGGPLMVIVEFCKFGNLSTY	927
Qy	939	LRAKRDAFSPCAEKSPEQGRGFRA---MVELARLDRRRPGSSDRVLFARFSKTEGGARRA	995
Db	928	LRSKRNEFVPTYKTG---ARFRQGDYVGAIPVDLKR--RLDSITSSQSSASSGFVEEK	981
Qy	996	S---PDQEA-EDLWLSPLTMEDLVCYSFQVARGMEFLASRKCIHRDLAARNILLSESDV	1050
Db	982	SLSDVEEEEAPELDYKDFLTLEHLICYSFQVAKGMEFLASRKCIHRDLAARNILLSEKNV	1041
Qy	1051	VKICDFGLARDIYKDPDYVRKGSARLPLKWMAPESIFDKVYTTQSDVWSFGVLLWEIFSL	1110
Db	1042	VKICDFGLARDIYKDPDYVRKGDARLPLKWMAPETIFDRVYTIQSDVWSFGVLLWEIFSL	1101
Qy	1111	GASPYPGVQINEEFQRLRDGTRMRAPLATPAIRIMLNCWSGDPKARPAFSELVEILG	1170
Db	1102	GASPYPGVKIDEEFCRRLKEGTRMRAPDYTTPEMYQTMDCWHGEPSQRPTFSELVEHLG	1161
Qy	1171	DLQGRGLQEHEEVCMAPRS-SQSSEGSFSQVSTMALHIAQADAEDSPPSLQRHSLAAR	1229
Db	1162	NLLQANAQQDGKDYIVLPISSETLSMEEDSGLSLPTSFPVSCMEHEEVCDP-----KFH	1213
Qy	1230	YYNWVSFPGCLARGAETRGSRRMKTFFEEP-TPPTYKGSVDNQTDSGMVLASEEFEQIE	1288
Db	1214	YDNTAGISQYLQNSKRKSRPVSVKTFEDIPLLEEPEVKVIPDDNQTDSGMVLASEELKTLE	1273
Qy	1289	SRHRQESGFSCKPGQNVAVTRAHPDSQGRRRRPERGARGGVFYNSEYGELESEPSEED	1347
Db	1274	DRTKLSPSFGGMVPSK---SRESVAEGSNQ-----TSGYQSGYHSDDTDTTVYSSEE	1323

RESULT 8

S09982

protein-tyrosine kinase (EC 2.7.1.112) flt1 precursor - human

N;Alternate names: receptor-type tyrosine kinase flt

C;Species: Homo sapiens (man)

C;Date: 12-Feb-1993 #sequence\_revision 12-Feb-1993 #text\_change 16-Aug-2004

C;Accession: S09982

R;Shibuya, M.; Yamaguchi, S.; Yamane, A.; Ikeda, T.; Tojo, A.; Matsushime, H.; Sato, M. Oncogene 5, 519-524, 1990

A;Title: Nucleotide sequence and expression of a novel human receptor-type tyrosine kinase gene (flt) closely related to the fms family.

A;Reference number: S09982; MUID:90221591; PMID:2158038

A;Accession: S09982

A;Molecule type: mRNA

A;Residues: 1-1338 <SHI>

A;Cross-references: UNIPROT:P17948; EMBL:X51602; NID:g31431; PIDN:CAA35946.1; PID:g31432

C;Genetics:

A;Gene: GDB:FLT1

A;Cross-references: GDB:120616; OMIM:165070

A;Map position: 13q12-13q12

C;Superfamily: protein kinase homology

C;Keywords: ATP; autophosphorylation; glycoprotein; membrane protein; phosphoprotein; phosphotransferase; tyrosine-specific protein kinase

F;1-22/Domain: signal sequence #status predicted <SIG>

F;23-1338/Product: protein-tyrosine kinase flt #status predicted <MAT>

F;825-1161/Domain: protein kinase homology <KIN>

F;833-841/Region: protein kinase ATP-binding motif

Query Match 34.2%; Score 2463; DB 2; Length 1338;  
Best Local Similarity 39.9%; Pred. No. 1.2e-103;  
Matches 547; Conservative 228; Mismatches 469; Indels 128; Gaps 28;

Qy 4 GAALCLRLWLCLGLLDGLVSGYSMTPTLNITEESHVIDTGDLSISICRGQHPLEWAWPG 63  
| | | | | | | | : | : : | : | : | : | : | :  
Db 8 GVLLC-ALLSCL-LLTGSSSGSKLKDPELSLKGTHIMQAGQTLHLQCRGEAAHKWS--- 62

Qy 64 AQEAPATGDKDSEDGTGVVRDCEGTDARPYCKVLLLHEVHANDTGSYVCYYKYIKARIEGT 123  
| : | : | : | : | : | : | : | : | : | : | : | :  
Db 63 ---LPEMVSKESERLSITKSACGRNGKQFCSTLTNLTAQANHTGFYSCKYLAVPTSKKKE 119

Qy 124 TAASSYVFVRDFEQPFINK----PDLLVNRKDMWVPCLVSIPLNVTLSR-QSSVLWP 178  
| : : | : | : | : | : | : | : | : | : | : | : | :  
Db 120 TESAIYIFISDTGRPFVEMYSEIPEIIHMTGRELVI PCRVTSNITVTLLKKFPLDTLIP 179

Qy 179 DGQEVVWDDRRGMLVSTPLLHDALYLQCETTWGDQDFLSNPFLVHITGNELYDIQLLPK 238  
| : : | : | : | : | : | : | : | : | : | : | : | :  
Db 180 DGKRIIWSRKGFIISNATYKEIGLLTCEATVNGHLYKTN-YLTHRQTNTIIDVQISTPR 238

Qy 239 SLELLVGEKLVLNCTVVAEFNSGVTFDWDYPGKAERGKWVPERRSQQTHTELS---SIL 295  
: : | | | | | | : | | | : : | | | : : : : | : |  
Db 239 PVKLLRGHTLVLNCTATTPLNTRVQMTWSYPDEKNKRAS--VRRRIDQSNSHANIFYSVL 296

Qy 296 TIHNVSQHDLGSYVCKANNGIQRFRESTEIVHENPFISVEWLKGPILEATAGDELVKLP 355  
| | : | | | | : | : | : | : | : | : | : | : | : |  
Db 297 TIDKMQNKDKGLYTCRVRSGPSFKSVNTSVHIYDKAFITVKHRKQVLETVAGKRSYRLS 356

Qy 356 VKLAAYPPPEFQWKDGKALSGRHS-----PHALVLKEVTEASTGTYYTLALWNSAAGLRR 410  
: : | : | | | : : : : : : : : : | : | : : : :  
Db 357 MKVKAFPSPEVWLKDGLPATEKSARYLTRGYSLIIDKDVTEEDAGNYTILLSIKQSNVFK 416

Qy 411 NISLELVVNVPPQIHEKEASS---PSIYSRHSRQALTCTAYGVPLPLSIQWHWRPWPCK 467  
| : : | : | | | : | | : : | | | | | : | : | : | : |  
Db 417 NLTATLIVNVKPKIYEKAVSSFPDPALYPLGSRQILTCTAYGIPQP-TIKWFHPCNHNH 475

Qy 468 MFAQRSLRRRQQQDLMPQCRDWRVATTQDAVNPIESLDTWTEFVEGKNKTVSKLVIQAN 527  
| : : : : : : | | | : : | | | | | : : : :  
Db 476 SEARCDFCSNNEESFILD-----ADSNMGNRIESITQRMALIEGKNKMASTLVVADSR 528

Qy 528 VSAMYKCVVSNKVGQDERLIYFYVTITPDGF--TIESKPSEELLEGQPVLLSCQADSYKY 585  
: | : | : | | | | | | : | : | : | : | : | : | : |



11	2681	37.2	1345	2	Q8VCD0	Q8vcd0	mus	musculu
12	2669	37.0	1367	1	VGR2_MOUSE	P35918	mus	musculu
13	2646	36.7	1343	1	VGR2_RAT	O08775	rattus	norv
14	2511	34.8	1327	2	Q8QHL3	Q8qhl3	gallus	gall
15	2469	34.2	1333	1	VGR1_MOUSE	P35969	mus	musculu
16	2463	34.2	1338	1	VGR1_HUMAN	P17948	h	vascular
17	2444.5	33.9	1336	1	VGR1_RAT	P53767	rattus	norv
18	2305	32.0	1302	1	VGR2_BRARE	Q8axb3	brachydanio	
19	1361	18.9	487	2	Q75WK4	Q75wk4	oryzias	lat
20	1283.5	17.8	367	2	Q91356	Q91356	coturnix	co
21	1181.5	16.4	1078	2	Q8AXC8	Q8axc8	fugu	rubrip
22	1163.5	16.1	1089	1	PGDS_HUMAN	P16234	homo	sapien
23	1160	16.1	1089	1	PGDS_MOUSE	P26618	mus	musculu
24	1158	16.1	1089	2	Q7TSJ3	Q7tsj3	mus	musculu
25	1151	16.0	1088	1	PGDS_RAT	P20786	rattus	norv
26	1150.5	16.0	1087	2	Q9PUF6	Q9puf6	gallus	
27	1134	15.7	1079	2	Q6E7G6	Q6e7g6	canis	famil
28	1128	15.6	404	2	Q9PUL0	Q9pul0	brachydanio	
29	1127	15.6	1474	2	Q8T4M0	Q8t4m0	drosophila	
30	1123.5	15.6	1087	2	Q7ZY71	Q7zy71	xenopus	lae
31	1122.5	15.6	1087	1	PGDS_XENLA	P26619	xenopus	lae
32	1118.5	15.5	1059	2	Q9DE49	Q9de49	brachydanio	
33	1117.5	15.5	1509	2	Q9VLQ8	Q9vqlq8	drosophila	
34	1117	15.5	1461	2	Q8T9F6	Q8t9f6	drosophila	
35	1113.5	15.4	1503	2	Q7KTI8	Q7kti8	drosophila	
36	1110.5	15.4	1509	2	Q8IPG1	Q8ipg1	drosophila	
37	1107.5	15.4	1509	2	Q95P10	Q95p10	drosophila	
38	1106.5	15.3	1503	2	Q8T4L8	Q8t4l8	drosophila	
39	1105	15.3	1062	2	Q8AXC7	Q8axc7	fugu	rubrip
40	1084	15.0	1103	2	Q6QNF3	Q6qnf3	canis	famil
41	1084	15.0	1106	1	PGDR_HUMAN	P09619	homo	sapien
42	1071.5	14.9	992	2	Q8AXU0	Q8axu0	oncorhynchu	
43	1070.5	14.8	977	2	Q98SU1	Q98su1	danio	nigro
44	1070	14.8	1383	2	Q7Q840	Q7q840	anopheles	g
45	1065	14.8	977	2	Q98SU4	Q98su4	danio	albol

# RESULT 2

## VGR3\_HUMAN

ID VGR3\_HUMAN STANDARD; PRT; 1298 AA.

AC P35916;

DT 01-JUN-1994 (Rel. 29, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 25-JAN-2005 (Rel. 46, Last annotation update)

DE Vascular endothelial growth factor receptor 3 precursor (EC 2.7.1.112)

DE (VEGFR-3) (Tyrosine-protein kinase receptor FLT4).

GN Name=FLT4;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A., AND VARIANTS GLN-890 AND HIS-1146.

RC TISSUE=Placenta;

RX MEDLINE=93241723; PubMed=8386825;

RA Galland F., Karamysheva A., Pebusque M.-J., Borg J.-P., Rottapel R.,

RA Dubreuil P., Rosnet O., Birnbaum D.;

RT "The FLT4 gene encodes a transmembrane tyrosine kinase related to the

RT vascular endothelial growth factor receptor.";

RL Oncogene 8:1233-1240(1993).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=93007958; PubMed=1327515;

RA Pajusola K., Aprelikova O., Korhonen J., Kaipainen A., Pertovaara L.,

RA Alitalo R., Alitalo K.;

RT "FLT4 receptor tyrosine kinase contains seven immunoglobulin-like

RT loops and is expressed in multiple human tissues and cell lines.";

RL Cancer Res. 52:5738-5743(1992).

RN [3]

RP ERRATUM.

RA Pajusola K., Aprelikova O., Korhonen J., Kaipainen A., Pertovaara L.,  
 RA Alitalo R., Alitalo K.;  
 RL Cancer Res. 53:3845-3845(1993).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RA Lee J., Gray A., Yuan J., Luoh S.M., Avraham H., Wood W.I.;  
 RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.  
 RN [5]  
 RP SEQUENCE OF 761-1190 FROM N.A.  
 RX MEDLINE=92119639; PubMed=1310071;  
 RA Aprelikova O., Pajusola K., Partanen J., Armstrong E., Alitalo R.,  
 RA Bailey S.K., McMahon J., Wasmuth J., Huebner K., Alitalo K.;  
 RT "FLT4, a novel class III receptor tyrosine kinase in chromosome 5q33-  
 RT qter.";  
 RL Cancer Res. 52:746-748(1992).  
 RN [6]  
 RP SEQUENCE OF 25-39.  
 RX PubMed=15340161; DOI=10.1110/ps.04682504;  
 RA Zhang Z., Henzel W.J.;  
 RT "Signal peptide prediction based on analysis of experimentally  
 RT verified cleavage sites.";  
 RL Protein Sci. 13:2819-2824(2004).  
 RN [7]  
 RP VARIANT HEREDITARY LYMPHEDEMA I LEU-1114.  
 RX PubMed=9817924; DOI=10.1093/hmg/7.13.2073;  
 RA Ferrell R.E., Levinson K.L., Esmen J.H., Kimak M.A., Lawrence E.C.,  
 RA Barmada M.M., Finegold D.N.;  
 RT "Hereditary lymphedema: evidence for linkage and genetic  
 RT heterogeneity.";  
 RL Hum. Mol. Genet. 7:2073-2078(1998).  
 RN [8]  
 RP INVOLVEMENT IN HEREDITARY LYMPHEDEMA I, AND CHARACTERIZATION OF  
 RP VARIANT HEREDITARY LYMPHEDEMA I ARG-1035.  
 RX PubMed=10856194;  
 RA Irrthum A., Karkkainen M.J., Devriendt K., Alitalo K., Vikkula M.;  
 RT "Congenital hereditary lymphedema caused by a mutation that  
 RT inactivates VEGFR3 tyrosine kinase.";  
 RL Am. J. Hum. Genet. 67:295-301(2000).  
 RN [9]  
 RP VARIANTS HEREDITARY LYMPHEDEMA I ARG-857; PRO-1041; PRO-1044 AND  
 RP LEU-1114, VARIANT SER-641, AND CHARACTERIZATION OF VARIANTS.  
 RX PubMed=10835628; DOI=10.1038/75997;  
 RA Karkkainen M.J., Ferrell R.E., Lawrence E.C., Kimak M.A.,  
 RA Levinson K.L., McTigue M.A., Alitalo K., Finegold D.N.;  
 RT "Missense mutations interfere with VEGFR-3 signalling in primary  
 RT lymphoedema.";  
 RL Nat. Genet. 25:153-159(2000).  
 RN [10]  
 RP VARIANTS JUVENILE HEMANGIOMA SER-954 AND SER-1137, AND VARIANTS  
 RP ALA-494; GLN-890 AND HIS-1146.  
 RX PubMed=11807987; DOI=10.1002/gcc.10028;  
 RA Walter J.W., North P.E., Waner M., Mizeracki A., Blei F.,  
 RA Walker J.W.T., Reinisch J.F., Marchuk D.A.;  
 RT "Somatic mutation of vascular endothelial growth factor receptors in  
 RT juvenile hemangioma.";  
 RL Genes Chromosomes Cancer 33:295-303(2002).  
 CC -!- FUNCTION: Receptor for VEGFC. Has a tyrosine-protein kinase  
 CC activity.  
 CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein  
 CC tyrosine phosphate.  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -!- TISSUE SPECIFICITY: Placenta, lung, heart, and kidney, does not  
 CC seem to be expressed in pancreas and brain.  
 CC -!- DISEASE: Defects in FLT4 are the cause of hereditary lymphedema I  
 CC [MIM:153100]; also known as Nonne-Milroy lymphedema or Milroy  
 CC disease. Hereditary lymphedema is a chronic disabling condition  
 CC which results in swelling of the extremities due to altered  
 CC lymphatic flow. Patients with lymphedema suffer from recurrent  
 CC local infections and physical impairment. Hereditary lymphedema I  
 CC shows autosomal dominant inheritance and is characterized by onset  
 CC usually at birth.

```

CC  -!- DISEASE: Defects in FLT4 are found in juvenile hemangioma.
CC      Juvenile hemangiomas are the most common tumors of infancy,
CC      occurring as many as 10/% of all births. These benign vascular
CC      lesions enlarge rapidly during the first year of life by
CC      hyperplasia of endothelial cells and attendant pericytes, and then
CC      spontaneously involute over a period of years, leaving loose
CC      fibrofatty tissue.
CC  -!- SIMILARITY: Belongs to the Tyr protein kinase family. CSF-1/PDGF
CC      receptor subfamily.
CC  -!- SIMILARITY: Contains 7 immunoglobulin-like C2-type domains.
CC  -----
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CC  the European Bioinformatics Institute. There are no restrictions on its
CC  use by non-profit institutions as long as its content is in no way
CC  modified and this statement is not removed. Usage by and for commercial
CC  entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC  or send an email to license@isb-sib.ch).
CC  -----
DR  EMBL; X69878; CAA49505.1; -.
DR  EMBL; X68203; CAA48290.1; ALT_INIT.
DR  EMBL; U43143; AAA85215.1; -.
DR  PIR; A48999; A48999.
DR  HSSP; P35968; 1VR2.
DR  Genew; HGNC:3767; FLT4.
DR  MIM; 136352; -.
DR  MIM; 153100; -.
DR  GO; GO:0005887; C:integral to plasma membrane; TAS.
DR  GO; GO:0005021; F:vascular endothelial growth factor receptor. . .; TAS.
DR  GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. . .; TAS.
DR  InterPro; IPR007110; Ig-like.
DR  InterPro; IPR003598; Ig_c2.
DR  InterPro; IPR011009; Kinase_like.
DR  InterPro; IPR000719; Prot_kinase.
DR  InterPro; IPR001824; RecepttyrkinsIII.
DR  InterPro; IPR001245; Tyr_pkinase.
DR  InterPro; IPR008266; Tyr_pkinase_AS.
DR  InterPro; IPR009134; VEGFR.
DR  InterPro; IPR009137; VEGFR3.
DR  Pfam; PF00047; ig; 6.
DR  Pfam; PF00069; Pkinase; 1.
DR  PRINTS; PR01832; VEGFRECEPTOR.
DR  PRINTS; PR01835; VEGFRECEPTR3.
DR  ProDom; PD000001; Prot_kinase; 2.
DR  SMART; SM00408; IGc2; 2.
DR  SMART; SM00219; TyrKc; 1.
DR  PROSITE; PSS0835; IG_LIKE; 6.
DR  PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR  PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR  PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR  PROSITE; PS00240; RECEPTOR_TYR_KIN_III; 1.
KW  ATP-binding; Direct protein sequencing; Disease mutation;
KW  Glycoprotein; Immunoglobulin domain; Phosphorylation; Polymorphism;
KW  Receptor; Repeat; Signal; Transferase; Transmembrane;
KW  Tyrosine-protein kinase.
FT  SIGNAL      1      24
FT  CHAIN       25    1298      Vascular endothelial growth factor
FT                                     receptor 3.
FT  DOMAIN      25      775      Extracellular (Potential).
FT  TRANSMEM    776      797      Potential.
FT  DOMAIN      798    1298      Cytoplasmic (Potential).
FT  DOMAIN      30     127      Ig-like C2-type 1.
FT  DOMAIN     151     213      Ig-like C2-type 2.
FT  DOMAIN     219     326      Ig-like C2-type 3.
FT  DOMAIN     331     415      Ig-like C2-type 4.
FT  DOMAIN     422     552      Ig-like C2-type 5.
FT  DOMAIN     555     671      Ig-like C2-type 6.
FT  DOMAIN     678     764      Ig-like C2-type 7.
FT  DOMAIN     845    1173      Protein kinase.
FT  NP_BIND     851     859      ATP (By similarity).
FT  BINDING     879     879      ATP (By similarity).

```

FT	ACT_SITE	1037	1037	By similarity.
FT	DISULFID	51	111	Potential.
FT	DISULFID	158	206	Potential.
FT	DISULFID	252	310	Potential.
FT	DISULFID	445	534	Potential.
FT	DISULFID	578	653	Potential.
FT	DISULFID	699	751	Potential.
FT	CARBOHYD	33	33	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	104	104	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	166	166	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	251	251	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	299	299	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	411	411	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	515	515	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	527	527	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	594	594	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	683	683	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	690	690	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	758	758	N-linked (GlcNAc. . .) (Potential).
FT	MOD_RES	1068	1068	Phosphotyrosine (by autocatalysis) (By similarity).
FT	VARIANT	494	494	T -> A.
FT				/FTId=VAR_018407.
FT	VARIANT	641	641	P -> S (does not affect kinase activity).
FT				/FTId=VAR_018408.
FT	VARIANT	857	857	G -> R (in hereditary lymphedema I; loss of kinase activity).
FT				

Query Match 95.0%; Score 6852; DB 1; Length 1298;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1297; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MQRGAALCLRLWLCLGLLDGLVSGYSMTPTLNITEESHVIDTGDSLISISCRGQHPLEWA	60
Db	1	MQRGAALCLRLWLCLGLLDGLVSGYSMTPTLNITEESHVIDTGDSLISISCRGQHPLEWA	60
Qy	61	WPGAQEAPATGDKDSED TGVRDCEGTDARPYCKVLLLEHVHANDTGSYVCYKYIKARI	120
Db	61	WPGAQEAPATGDKDSED TGVRDCEGTDARPYCKVLLLEHVHANDTGSYVCYKYIKARI	120
Qy	121	EGTTAASSYVFVRDFEQPFINKPDTLLVNRKDMWVPCLVSIPLNVTLRSSSVLWPDG	180
Db	121	EGTTAASSYVFVRDFEQPFINKPDTLLVNRKDMWVPCLVSIPLNVTLRSSSVLWPDG	180
Qy	181	QEVVWDDRRGMLVSTPLLDALYLQCETTWGDQDFLSNPFLVHITGNELYDIQLLPKRSK	240
Db	181	QEVVWDDRRGMLVSTPLLDALYLQCETTWGDQDFLSNPFLVHITGNELYDIQLLPKRSK	240
Qy	241	ELLVGEKLVNLCTVWAEFNSGVTFDWDYPGKQAERGKWVPERRSQQTHTELSSILTIHNV	300
Db	241	ELLVGEKLVNLCTVWAEFNSGVTFDWDYPGKQAERGKWVPERRSQQTHTELSSILTIHNV	300
Qy	301	SQHDLGSYVCKANNGIQRFRESTEVIHNPFI SVEWLKGPILEATAGDELVKLPVKLAA	360
Db	301	SQHDLGSYVCKANNGIQRFRESTEVIHNPFI SVEWLKGPILEATAGDELVKLPVKLAA	360
Qy	361	YPPPEFQWKDGKALSGRHS PHALVLKEVTEASTGT YTLALWNSAAGLRRNISLELVNV	420
Db	361	YPPPEFQWKDGKALSGRHS PHALVLKEVTEASTGT YTLALWNSAAGLRRNISLELVNV	420
Qy	421	PPQIHEKEASSPSIYSRHSRQALTCTAYGVPLPLSIQWHWPWPCKMFAQRS LRRRQQQ	480
Db	421	PPQIHEKEASSPSIYSRHSRQALTCTAYGVPLPLSIQWHWPWPCKMFAQRS LRRRQQQ	480
Qy	481	DLMPQCRDWRVATTQDAVNPIESLDTWTEFVEGKNKTVSKLVIQANANVSAMYKCVVSNKV	540
Db	481	DLMPQCRDWRVATTQDAVNPIESLDTWTEFVEGKNKTVSKLVIQANANVSAMYKCVVSNKV	540
Qy	541	GQDERLIYFYVTTIPDGFTIESKPSEELLEGQPVLLSCQADSYKYEHLRWYRLNLSLTHD	600
Db	541	GQDERLIYFYVTTIPDGFTIESKPSEELLEGQPVLLSCQADSYKYEHLRWYRLNLSLTHD	600

Qy	601	AHGNPLLLDCKNVHLFATPLAASLEEVPAGARHATLSLSIPRVAPEHEGHYVCEVQDRRS	660
Db	601	AHGNPLLLDCKNVHLFATPLAASLEEVPAGARHATLSLSIPRVAPEHEGHYVCEVQDRRS	660
Qy	661	HDKHCHKKYLSVQALEAPRLTQNLTDLLVNVSDSLEMQCLVAGAHAPSIVWYKDERLLEE	720
Db	661	HDKHCHKKYLSVQALEAPRLTQNLTDLLVNVSDSLEMQCLVAGAHAPSIVWYKDERLLEE	720
Qy	721	KSGVDLADSNQKLSIQRVREEDAGRYLCSVCNAKGCVNSSASVAVEGSEDKGSMEIVILV	780
Db	721	KSGVDLADSNQKLSIQRVREEDAGRYLCSVCNAKGCVNSSASVAVEGSEDKGSMEIVILV	780
Qy	781	GTGVIAVFFWVLLLLIFCNMRRPAHADIKTGYSIIMDPGEVPLEEQCEYLSYDASQWEF	840
Db	781	GTGVIAVFFWVLLLLIFCNMRRPAHADIKTGYSIIMDPGEVPLEEQCEYLSYDASQWEF	840
Qy	841	PRERLHLGRVLGYGAFGKVVEASAFGIHKGSSCDTVAVKMLKEGATASEHRALMSELKIL	900
Db	841	PRERLHLGRVLGYGAFGKVVEASAFGIHKGSSCDTVAVKMLKEGATASEHRALMSELKIL	900
Qy	901	IHIGNHLNVVNLGACTKPQGPLMVIVEFCKYGNLSNFLRAKRDAFSPCAEKSPEQRGRF	960
Db	901	IHIGNHLNVVNLGACTKPQGPLMVIVEFCKYGNLSNFLRAKRDAFSPCAEKSPEQRGRF	960
Qy	961	RAMVELARLDRRRPGSSDRVLFARFSKTEGGARRASPDQEAEDLWLSPLTMEDLVCYSFQ	1020
Db	961	RAMVELARLDRRRPGSSDRVLFARFSKTEGGARRASPDQEAEDLWLSPLTMEDLVCYSFQ	1020
Qy	1021	VARGMEFLASRKCIHRDLAARNILLSSESDVVKICDFGLARDIYKDPDYVRKGSARLPLKW	1080
Db	1021	VARGMEFLASRKCIHRDLAARNILLSSESDVVKICDFGLARDIYKDPDYVRKGSARLPLKW	1080
Qy	1081	MAPESIFDKVYTTQSDVWSFGVLLWEIFSLGASPYPGVQINEEFCQRLRDGTRMRAPELA	1140
Db	1081	MAPESIFDKVYTTQSDVWSFGVLLWEIFSLGASPYPGVQINEEFCQRLRDGTRMRAPELA	1140
Qy	1141	TPAIRRIMLNCWSGDPKARPAFSELVEILGDLQGRGLQEEEEVCMAPRSSQSSEEGSFS	1200
Db	1141	TPAIRRIMLNCWSGDPKARPAFSELVEILGDLQGRGLQEEEEVCMAPRSSQSSEEGSFS	1200
Qy	1201	QVSTMALHIAQADAEDSPPSLQRHSLAARYYNWVSFPGCLARGAETRGSSRMKTFEFPM	1260
Db	1201	QVSTMALHIAQADAEDSPPSLQRHSLAARYYNWVSFPGCLARGAETRGSSRMKTFEFPM	1260
Qy	1261	TPTTYKGSVDNQTDSGMVLASEEFEQIESRHRQESGF	1297
Db	1261	TPTTYKGSVDNQTDSGMVLASEEFEQIESRHRQESGF	1297

# RESULT 10

## VGR2\_HUMAN

ID VGR2\_HUMAN STANDARD; PRT; 1356 AA.  
AC P35968; O60723; Q14178;  
DT 01-JUN-1994 (Rel. 29, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 25-OCT-2004 (Rel. 45, Last annotation update)  
DE Vascular endothelial growth factor receptor 2 precursor (EC 2.7.1.112)  
DE (VEGFR-2) (Kinase insert domain receptor) (Protein-tyrosine kinase  
DE receptor Flk-1).  
GN Name=KDR; Synonyms=FLK1;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Yin L.Y., Wu Y., Patterson C.;  
RT "Full length human KDR/flk-1 sequence."  
RL Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.  
RN [2]



RP SEQUENCE FROM N.A.  
 RC TISSUE=Umbilical vein;  
 RA Yu Y., Whitney R.G., Sato J.D.;  
 RT "Coding region for human VEGF receptor KDR (VEGFR-2).";  
 RL Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.  
 RN [3]  
 RP SEQUENCE OF 3-1356 FROM N.A.  
 RC TISSUE=Umbilical vein;  
 RX MEDLINE=92019839; PubMed=1656371;  
 RA Terman B.I., Carrion M.E., Kovacs E., Rasmussen B.A., Eddy R.L.,  
 RA Shows T.B.;  
 RT "Identification of a new endothelial cell growth factor receptor  
 RT tyrosine kinase.";  
 RL Oncogene 6:1677-1683(1991).  
 RN [4]  
 RP SEQUENCE OF 1-22 FROM N.A.  
 RX MEDLINE=96032749; PubMed=7559454; DOI=10.1074/jbc.270.39.23111;  
 RA Patterson C., Perrella M.A., Hsieh C.M., Yoshizumi M., Lee M.E.,  
 RA Harber E.;  
 RT "Cloning and functional analysis of the promoter for KDR/flk-1, a  
 RT receptor for vascular endothelial growth factor.";  
 RL J. Biol. Chem. 270:23111-23118(1995).  
 RN [5]  
 RP FUNCTION.  
 RX MEDLINE=93038639; PubMed=1417831;  
 RA Terman B.I., Dougher-Vermazen M., Carrion M.E., Dimitrov D.,  
 RA Armellino D.C., Gospodarowicz D., Boehlen P.;  
 RT "Identification of the KDR tyrosine kinase as a receptor for vascular  
 RT endothelial cell growth factor.";  
 RL Biochem. Biophys. Res. Commun. 187:1579-1586(1992).  
 CC -!- FUNCTION: Receptor for VEGF or VEGFC. Has a tyrosine-protein  
 CC kinase activity. The VEGF-kinase ligand/receptor signaling system  
 CC plays a key role in vascular development and regulation of  
 CC vascular permeability.  
 CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein  
 CC tyrosine phosphate.  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -!- SIMILARITY: Belongs to the Tyr protein kinase family. CSF-1/PDGF  
 CC receptor subfamily.  
 CC -!- SIMILARITY: Contains 7 immunoglobulin-like C2-type domains.  
 CC -----  
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 CC -----  
 DR EMBL; AF035121; AAB88005.1; -.  
 DR EMBL; AF063658; AAC16450.1; -.  
 DR EMBL; X61656; CAA43837.1; -.  
 DR EMBL; L04947; AAA59459.1; -.  
 DR EMBL; X89776; CAA61916.1; -.  
 DR PIR; JC1402; JC1402.  
 DR PDB; 1VR2; X-ray; A=806-1171.  
 DR Genew; HGNC:6307; KDR.  
 DR MIM; 191306; -.  
 DR GO; GO:0005887; C:integral to plasma membrane; TAS.  
 DR GO; GO:0005021; F:vascular endothelial growth factor receptor. . .; TAS.  
 DR GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. . .; TAS.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003598; Ig\_c2.  
 DR InterPro; IPR011009; Kinase\_like.  
 DR InterPro; IPR000719; Prot\_kinase.  
 DR InterPro; IPR001824; RecepttyrkinsIII.  
 DR InterPro; IPR001245; Tyr\_pkinase.  
 DR InterPro; IPR008266; Tyr\_pkinase\_AS.  
 DR InterPro; IPR009134; VEGFR.  
 DR InterPro; IPR009136; VEGFR2.  
 DR Pfam; PF00047; ig; 6.

DR	Pfam; PF00069; Pkinase; 1.
DR	PRINTS; PR01832; VEGFRECEPTOR.
DR	PRINTS; PR01834; VEGFRECEPTR2.
DR	ProDom; PD000001; Prot_kinase; 2.
DR	SMART; SM00408; IGc2; 2.
DR	SMART; SM00219; TyrKc; 1.
DR	PROSITE; PS50835; IG_LIKE; 5.
DR	PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR	PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR	PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR	PROSITE; PS00240; RECEPTOR_TYR_KIN_III; 1.
KW	3D-structure; Angiogenesis; ATP-binding; Glycoprotein;
KW	Immunoglobulin domain; Phosphorylation; Receptor; Repeat; Signal;
KW	Transferase; Transmembrane; Tyrosine-protein kinase.
FT	SIGNAL 1 19 Potential.
FT	CHAIN 20 1356 Vascular endothelial growth factor receptor 2.
FT	DOMAIN 20 764 Extracellular (Potential).
FT	TRANSMEM 765 789 Potential.
FT	DOMAIN 790 1356 Cytoplasmic (Potential).
FT	DOMAIN 46 110 Ig-like C2-type 1.
FT	DOMAIN 141 207 Ig-like C2-type 2.
FT	DOMAIN 224 320 Ig-like C2-type 3.
FT	DOMAIN 328 414 Ig-like C2-type 4.
FT	DOMAIN 421 548 Ig-like C2-type 5.
FT	DOMAIN 551 660 Ig-like C2-type 6.
FT	DOMAIN 667 753 Ig-like C2-type 7.
FT	DOMAIN 834 1162 Protein kinase.
FT	NP_BIND 840 848 ATP (By similarity).
FT	BINDING 868 868 ATP (By similarity).
FT	ACT_SITE 1028 1028 By similarity.
FT	CARBOHYD 46 46 N-linked (GlcNAc . . .) (Potential).
FT	CARBOHYD 66 66 N-linked (GlcNAc . . .) (Potential).
FT	CARBOHYD 96 96 N-linked (GlcNAc . . .) (Potential).
FT	CARBOHYD 143 143 N-linked (GlcNAc . . .) (Potential).
FT	CARBOHYD 158 158 N-linked (GlcNAc . . .) (Potential).
FT	CARBOHYD 245 245 N-linked (GlcNAc . . .) (Potential).
FT	CARBOHYD 318 318 N-linked (GlcNAc . . .) (Potential).
FT	CARBOHYD 374 374 N-linked (GlcNAc . . .) (Potential).
FT	CARBOHYD 395 395 N-linked (GlcNAc . . .) (Potential).
FT	CARBOHYD 511 511 N-linked (GlcNAc . . .) (Potential).
FT	CARBOHYD 523 523 N-linked (GlcNAc . . .) (Potential).
FT	CARBOHYD 580 580 N-linked (GlcNAc . . .) (Potential).
FT	CARBOHYD 613 613 N-linked (GlcNAc . . .) (Potential).
FT	CARBOHYD 619 619 N-linked (GlcNAc . . .) (Potential).
FT	CARBOHYD 631 631 N-linked (GlcNAc . . .) (Potential).
FT	CARBOHYD 675 675 N-linked (GlcNAc . . .) (Potential).
FT	CARBOHYD 704 704 N-linked (GlcNAc . . .) (Potential).
FT	CARBOHYD 721 721 N-linked (GlcNAc . . .) (Potential).
FT	MOD_RES 1059 1059 Phosphotyrosine (by autocatalysis) (By similarity).
FT	CONFLICT 2 2 Q -> E (in Ref. 2).
FT	CONFLICT 772 772 A -> T (in Ref. 3).
FT	CONFLICT 787 787 R -> G (in Ref. 3).
FT	CONFLICT 835 835 K -> N (in Ref. 3).
FT	CONFLICT 848 848 V -> E (in Ref. 3).
FT	CONFLICT 1347 1347 S -> T (in Ref. 3).
SQ	SEQUENCE 1356 AA; 151526 MW; 59E7C44B05CFEBB3 CRC64;
Query Match 38.3%; Score 2762; DB 1; Length 1356;	
Best Local Similarity 44.1%; Pred. No. 8.5e-172;	
Matches 608; Conservative 203; Mismatches 480; Indels 88; Gaps 26;	
Qy	1 MQRGAALCLRLWLCLGLLDGLVS--GYSMTPPTLNITEESHVIDTGDLSLSISCRGQHPL 58     :       :   :  :  :  :  :  :  :  :
Db	1 MQSKVLLAVALWLCVETRAASVGLPSVSLDLPRLSIQKDILTIKANITLQITCRGQRDL 60
Qy	59 WAWPGAQEAPATGDKDSED TGVRDC-EGTDARPYCVLLLHEVHANDGSYVCYKYIK 117     :     :  :  :  :  :  :  :  :  :  :  :
Db	61 WLWPNNOSG-----SEORVEVTECS DGL----FCKTLTI PKVIGNDTGAYKCFYR--- 106

Qy	118	ARIEGITAATAASSYVFRDFEQPFINKPDT-----LLVNRKMDAMWVPCLVISPLGNVTL--	169
Db	107	---ETDLASVIYVYVQDYRSPFIASVSDQHGVVYITENKNKTVVIPCGLGISNLNVSLCA	163
Qy	170	RSQSSVLWPDGQEVVWDDRRGMLVSTPLLDHALYLQCETTWDGQDFLSNPFLVHITGNEL	229
Db	164	RYPEKRFVPDGNRISWDSKKGFTIPSYMISYAGMVFCIAKINDESYQSIMYIVVVVGRI	223
Qy	230	YDIQLLPKRSLELLVGEKLVLNCTVWAEFNSGVTFDWDYPGKQAERGKWVPERRSQQHT	289
Db	224	YDVVLSPSHGIELSVGEKLVLNCTARTELVNIGIDFNWEYPPSSKHQHKLVNRDLKTQSGS	283
Qy	290	ELS---SILTIHNVSQHDLGSYVCKANNGIQRFRESTEVIHVENPFISVEWLKGPILEAT	346
Db	284	EMKKFLSTLTIDGVTRSDQGLYTCAASSGLMTKKNSTFVRVHEKPFVAFGSGMESLVEAT	343
Qy	347	AGDELVLKLPVKLAAYPPPEFQWYKDGKALSGRH---SPHALVLKEVTEASTGTITLALWN	403
Db	344	VG-ERVRIPAKYLGYPPPEIKWYKNGIPLESNHTIKAGHVLTIMEVSRDGTGNYTVILT	402
Qy	404	SAAGLRRNISLELVVNVPPIHEKEASSP-SIYSRHSRQALCTAYGVPLPLSIQWHWRP	462
Db	403	PISKEKQSHVSVLVVYVPPQIGEKSLISPVDSYQYGTQTTLCTVYAIPPPHIHWWYQL	462
Qy	463	WTPCKMFAQRSLRRRQQQDLMPQCRDRAVTTQDAVNPIESLDTWTVEFVEGKNKTVSKLV	522
Db	463	EEEC---ANEPSQAVSVTNPYP-CEEWSVEDFQGGNKIEVNKNQFALIEGKNKTVSTLV	518
Qy	523	IQNANVSAMYKCVVSNKVGQDERLIYFVTTIPDGFTIESKPSEELLEGGQPVLLSCQADS	582
Db	519	IQAANVSALYKCEAVNKVGRGERVISFHVTRGPE---ITLQPDMPTEQESVSLWCTADR	575
Qy	583	YKYEHLRWYRLNLSTLHDAHGNPLLLDCKNV---HLFATPLAASLEEVAPGARHATLSL	638
Db	576	STFENLTWYKLGPOPLPIHVGEPLTPVCKNLDTLWKLNATMFSNSTNDI-----LIM	627
Qy	639	SIPRVAPEHEGHYVCEVQDRRSHDKHKCHKYLSVQALEAPRLTQNLDTLLVNVSDSLEMQ	698
Db	628	ELKNASLQDQGDYVCLAQDRKTKKRHCVVRLTVLRLVAPTITGNLENQTTSIGESIEVS	687
Qy	699	CLVAGAHAPSIWYKDERLLEEKSGVDLADSNQKLSIQRVREEDAGRYLCSVCNAKGCVN	758
Db	688	CTASGNPPPQIMWFKDNETLVEDSGIVLKDGNRNLTIRVRKEDEGLYTCQACSVLGCAK	747
Qy	759	SSASVAVEGSEDKGSMEIVILVGTGVIAVFFWVLLLLIFCNMRRPAHADIKTGYSIIMD	818
Db	748	VEAFFIIEBGAQKTNLEIIILVGTAVIAMFFWVLLVILRTVKRANGGELKTGYLSIVMD	807
Qy	819	PGEVPLEEQCEYLSYDASQWEFPRERLHLGRVLGYGAFGKVVEASAFGIHKSSCDTVAV	878
Db	808	PDELPLDEHCERLPYDASKWEFPRDLRLKGLKPLGRGAFQGVIEADAFGIDKTATCRTVAV	867
Qy	879	KMLKEGATASEHRALMSELKILIHIGHNLNVNLLGACTKPGQPLMVIVEFCKYGNLSNF	938
Db	868	KMLKEGATHSEHRALMSELKILIHIGHHLNVNLLGACTKPGGPLMVIVEFCKFGNLSTY	927
Qy	939	LRAKRDAFSPCAEKSPQGRGFRA---MVELARLDRRRPGSSDRVLFAFBSKTEGGARRA	995
Db	928	LSKRNEFVPYKTKG----ARFRQGDYVGAIPVDLKR--RLDSITSSQSSASSGFVEEK	981
Qy	996	S----PDQEA-EDLWLSPLTMEDLVCSYFQVARGMEFLASRKCIHRDLAARNILLSESDV	1050
Db	982	SLSDVEEEEAPEDLYKDFLTLEHLICYSFQVAKGMEFLASRKCIHRDLAARNILLSEKNV	1041
Qy	1051	VKICDFGLARDIYKDPDYVRKGSARLPLKWMAPESIFDKVYTTQSDVWSFGVLLWEIFSL	1110
Db	1042	VKICDFGLARDIYKDPDYVRKGDARLPLKWMAPETIFDRVYTIQSDVWSFGVLLWEIFSL	1101
Qy	1111	GASPYPGVQINEEFCQRLRDGTRMAPELATPAIRIMLNCWSGDPKARPAFSELVEILG	1170
Db	1102	GASPYPGVKIDEEFCRLKEGTRMRAPDYTTPEMYQTMLCDWHGEPSPORPTFSELVEHLG	1161



RT factor and is selectively expressed in vascular endothelium.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 90:7533-7537(1993).  
 CC -!- FUNCTION: Receptor for VEGF or VEGFC. Has a tyrosine-protein  
 CC kinase activity. The VEGF-kinase ligand/receptor signaling system  
 CC plays a key role in vascular development and regulation of  
 CC vascular permeability.  
 CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein  
 CC tyrosine phosphate.  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -!- TISSUE SPECIFICITY: Expressed at high levels in adult heart, lung,  
 CC kidney, brain and skeletal muscle, but is also expressed at lower  
 CC levels in most other adult tissues.  
 CC -!- SIMILARITY: Belongs to the Tyr protein kinase family. CSF-1/PDGF  
 CC receptor subfamily.  
 CC -!- SIMILARITY: Contains 7 immunoglobulin-like C2-type domains.  
 CC -----  
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 CC -----  
 DR EMBL; X70842; CAA50192.1; -.  
 DR EMBL; X59397; CAA42040.1; -.  
 DR EMBL; S53103; AAB25043.1; -.  
 DR EMBL; X89777; CAA61917.1; -.  
 DR PIR; A41228; A41228.  
 DR HSSP; P35968; 1VR2.  
 DR MGD; MGI:96683; Kdr.  
 DR GO; GO:0045165; P:cell fate commitment; IMP.  
 DR GO; GO:0045446; P:endothelial cell differentiation; IDA.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003598; Ig\_c2.  
 DR InterPro; IPR011009; Kinase\_like.  
 DR InterPro; IPR000719; Prot\_kinase.  
 DR InterPro; IPR001824; RecepttyrkinsIII.  
 DR InterPro; IPR001245; Tyr\_pkinase.  
 DR InterPro; IPR008266; Tyr\_pkinase\_AS.  
 DR InterPro; IPR009134; VEGFR.  
 DR InterPro; IPR009136; VEGFR2.  
 DR Pfam; PF00047; ig; 6.  
 DR Pfam; PF00069; Pkinase; 1.  
 DR PRINTS; PR01832; VEGFRECEPTOR.  
 DR PRINTS; PR01834; VEGFRECEPTR2.  
 DR ProDom; PD000001; Prot\_kinase; 2.  
 DR SMART; SM00408; IGc2; 1.  
 DR SMART; SM00219; TyrKc; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 5.  
 DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE; PS00109; PROTEIN\_KINASE\_TYR; 1.  
 DR PROSITE; PS00240; RECEPTOR\_TYR\_KIN\_III; 1.  
 KW Angiogenesis; ATP-binding; Glycoprotein; Immunoglobulin domain;  
 KW Phosphorylation; Receptor; Repeat; Signal; Transferase; Transmembrane;  
 KW Tyrosine-protein kinase.  
 FT SIGNAL 1 19 Potential.  
 FT CHAIN 20 1367 Vascular endothelial growth factor  
 FT receptor 2.  
 FT DOMAIN 20 762 Extracellular (Potential).  
 FT TRANSMEM 763 784 Potential.  
 FT DOMAIN 785 1367 Cytoplasmic (Potential).  
 FT DOMAIN 46 111 Ig-like C2-type 1.  
 FT DOMAIN 143 209 Ig-like C2-type 2.  
 FT DOMAIN 226 325 Ig-like C2-type 3.  
 FT DOMAIN 330 416 Ig-like C2-type 4.  
 FT DOMAIN 423 542 Ig-like C2-type 5.  
 FT DOMAIN 549 656 Ig-like C2-type 6.  
 FT DOMAIN 665 751 Ig-like C2-type 7.  
 FT DOMAIN 832 1160 Protein kinase.

FT	NP_BIND	838	846	ATP (By similarity).
FT	BINDING	866	866	ATP (By similarity).
FT	ACT_SITE	1026	1026	By similarity.
FT	CARBOHYD	46	46	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	98	98	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	145	145	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	160	160	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	247	247	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	320	320	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	376	376	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	397	397	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	509	509	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	521	521	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	578	578	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	611	611	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	617	617	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	629	629	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	673	673	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	702	702	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	719	719	N-linked (GlcNAc. . .) (Potential).
FT	MOD_RES	1057	1057	Phosphotyrosine (by autocatalysis) (By similarity).
FT	CONFLICT	25	25	P -> T (in Ref. 1).
FT	CONFLICT	679	679	G -> D (in Ref. 3).
FT	CONFLICT	783	784	LV -> VL (in Ref. 1).
FT	CONFLICT	917	917	S -> C (in Ref. 1).
FT	CONFLICT	1341	1367	QLTSCLNGSGVPVAPPPTPGNHERGAA -> RSPPV (in Ref. 3).
SQ	SEQUENCE	1367 AA;	152516 MW;	EFC99704F1DCA266 CRC64;

Query Match 37.0%; Score 2669; DB 1; Length 1367;  
 Best Local Similarity 43.0%; Pred. No. 1.1e-165;  
 Matches 588; Conservative 205; Mismatches 485; Indels 90; Gaps 24;

Qy	1	MQRGAALCLRLWLCLGLLDGLVS--GYSMTPPTLNITEESHVIDTGDSLISISCRGQHPLE	58
Db	1	MESKALLAVALWFCVETRAASVGLPGDFLHPPKLSTQKDILTILANTTLQITCRGQRDL	60
Qy	59	WAWPGAQEAPATGDKDSED TG VVRDC EGT DARPYCKVLLLHEVHANDTGSYVCYKYIKA	118
Db	61	WLWPNAQ-----RDSEERVLVTECGGDS-IFCKTLTIPRVVGN DTGAYKCSYRDV--	110
Qy	119	RIEGTTAASSYVVRDFEQPFINKPDT-----LLVNRKDMWVPCLVSIPLGNVTL--R	170
Db	111	----DIAS TVYVVRDYRSPFIASVSDQHGI VYITENKNKT VVIPCRGSISNLNVSLCAR	166
Qy	171	SQSSVLWPDGQEVVWDDRRGMLVSTPLLHDALYLQCE TTWGDQDFLSNPFLVHITGNELY	230
Db	167	YPEKRFPVDPGNRISWDSEIGFTLPSYMISYAGMV FCEAKINDETYQSIMYIVVVGYRIY	226
Qy	231	DIQLLPKRSLELLVGEKLVLNCTVWAEFNSGVTFDWDYPGKQAERGKWVPERRSQQTHT	290
Db	227	DVILSPPHIEI LSAGEKLVLNCTARTELVGLDFTWHSPPSKSHHKI VNRDVKPFPGTV	286
Qy	291	LS---SILTIHNVSQHDLGSYVCKANNGIQRFRESTEVI VHENPFISVEWLKGPILEATA	347
Db	287	AKMFLSTLTIESVT KSDQGEYTCVASSGRMIKRNTFVRVHTKPFIAFGSGMKSLVEATV	346
Qy	348	GDELVKLPVKLAAYPPPEFQWKDGKALSGRHS---PHALVLKEVTEASTGT YTLALWNS	404
Db	347	GSQ-VRI PVKYLSPAPDIKWYRNGRPIESNYTMIVGDELTIMEVTERDAGNYTVILTNP	405
Qy	405	AAGLRNINISLELVVNVPPIHEKEASSP-SIYSRHSRQALTCTAYGVPLPLSIQWHWRPW	463
Db	406	ISMEKQSHMVSLVVNVPPQIGEKALISPMDSYQYGTMQTLTCTVYANPPLHHIQWYQLE	465
Qy	464	TPCKMFAQRSLRRRQQQLMPQCRDWRAVTTQDAVNPIESLDTWTEFVEGKNKTVSKLVI	523
Db	466	EACSY-----RPGQTS PYACKEWRHVEDFQGGNKIEVTKNQYALIEGKNKTVSTLVI	517
Qy	524	QNANVSAMKYCVVSNKVGQDERLIYFVYVTTIPDGFTIESKPSEELLEGPVLLSCQADSY	583

Db	518	QAANVSALYKCEAINKAGRGERSVISFHVIRGPE---ITVQPAAQPTQESVSLLCTADRN	574
Qy	584	KYEHLRWYRLNLSTLHDAHGNPLLLDCKNV---HLFATPLAASLEEVAPGARHATLSLS	639
Db	575	TFENLTWYKLSQATSVMHGESLTPVCKNLDALWKLNGTMFSNSTNDI-----LIVA	626
Qy	640	IPRVAPEHEGHYVCEVQDRRSHDKHCHKYLSVQALEAPRLTQNLTDLLVNVSDSLEMQC	699
Db	627	FQNASLQDQGDYVCSAQDKKTKKRHCLVKQLIILERMAPMITGNLENQTTTIGETIEVTC	686
Qy	700	LVAGAHAPSIVWYKDERLLEEKSGVDLADSNQKLSIQRVREEDAGRYLCSVCNAKGCVNS	759
Db	687	PASGNPTPHITWFKDNETLVEDSGIVLRDGNRNLTIRRVKEDGGLYTCQACNVLCARA	746
Qy	760	SASVAVEGSEDKGSMEIVILVGTGVIAVFFWVLLLLIFCNMRRPAHADIKTYLSIIMDP	819
Db	747	ETLFIIEGAQEKTNLEVIILVGTAVIAMFFWVLLLLVILVRTVKRANEGELKTGYLSIVMDP	806
Qy	820	GEVPLEEQCEYLSYDASQWEFPRERLHLGRVLGYGAFGKVVEASAFGIHKSSCDTVAVK	879
Db	807	DEPLDERCERLPYDASKWEFPRDLKLGKPLGRGAFGQVIEADAFGIDKTATCKTVAVK	866
Qy	880	MLKEGATASEHRALMSELKILIHIGNHLNVNLLGACTKPQGPLMVIVEFCKYGNLSNFL	939
Db	867	MLKEGATHSEHRALMSELKILIHIGHHLNVNLLGACTKPGGPLMVIVEFSKFGNLSTYL	926
Qy	940	RAKRDAFSPCAEKSPEQRGRFRA---MVELARLDRRRPGSSDRVLFARFSKTEGGARRA	995
Db	927	RGKRNEFVVPYKSG---ARFRQGDYVGELS-VDLKR--RLDSITSSQSSASSGFVEEK	979
Qy	996	S-----PDQEAEDLWLSPLTMEDLVCYSFQVARGMEFLASRKCIHRDLAARNILLSSESDV	1050
Db	980	SLSDVEEEEASEELYKDFLTLEHLICYSFQVAKGMEFLASRKCIHRDLAARNILLSSEKNV	1039
Qy	1051	VKICDFGLARDIYKDPDYVRKGSARLPLKWMAPESIFDKVYTTQSDVWSFGVLLWEIFSL	1110
Db	1040	VKICDFGLARDIYKDPDYVRKG DARLPLKWMAPETIFDRVYTIQSDVWSFGVLLWEIFSL	1099
Qy	1111	GASPYPGVQINEEFCQRLRDGTRMRAPELATPAIRRIMLNCWSGDPKARPAFSELVEILG	1170
Db	1100	GASPYPGVKIDEEFCRRLKEGTRMRAPDYTTPEMYQTMLDCHWEDPNQRPSFSELVEHLG	1159
Qy	1171	DLQGRGLQEEEEVCMAPRS-SQSSEEGSFSQVSTMALHIAQADAEDSPPSLQRHSLAAR	1229
Db	1160	NLLQANAQQDGKDYIVLPMSETLSMEEDSGLSLPTSPVSCMEEEEVCDP-----KPH	1211
Qy	1230	YNNWVSFPGCLARGAETRGSRRMKTFFEEFPM-TPTTYKGSVDNQTDSGMVLASEEFEQIE	1288
Db	1212	YDNTAGISHYLQNSKRKSRPVSVKTFEDIPLLEEPEVKVIPDDSQTDSGMVLASEELKTLE	1271
Qy	1289	SRHRQESGFSCKPGQNNAVTRAHPDSQGRRRRPERGARGGQVFYNSE	1336
Db	1272	DRNKLSPSFG---GMMPKSRESVASEGSNQ-----TSGYQSGYHSD	1310